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# FIG.1A

## Human Glial Cell Line-Derived Neurotrophic Factor Receptor Protein

10	30	50
AATCTGGCCTCGGAACACAGCCATTCTCCGCGCGCTTCCAATAACCACATAACATCCCTA		
70	90	110
ACGAGCATCCGAGCCGAGGGCTCTGCTCGGAAATCGTCTGGCCCAACTCGGCCCTTCGA		
130	150	170
GCTCTCGAAGATTACCGCATCTATTTTTTTTCTTTTTTTTCTTTTCTTTCTTAGCGCAGATA		



## FIG.1B

190	210	230
AAGTGAGCCCGGAAGGGAAGGAGGGGGGACACCATTTGCCCTGAAAGAAATAATAA		
250	270	290
GTAAATAACAACTGGCTCCTCGCCGACGTGGACGGGTCGGTTGAGTCCAGGTTGGG		
310	330	350
TCGGACCTGAACCCCTAAAGCGGAACCGCCTCCCGCCCTCGCCATCCCGGAGCTGAGTC		
370	390	410
GCCGGCGCGGTGGCTGCTGCCAGACCCGGAGTTTCCTCTTCACTGGATGGAGCTGAAC		



## FIG.1C

430	450	470																	
TTTGGGGCCAGAGCAGCACAGCTGTCCGGGGATCGCTGCACGCTGAGCTCCCTCGGCA																			
490	510	530																	
AGACCCAGCGCGGCTCGGGATTTTTGGGGGGGGGACCAAGCCCCGGCCGGCACC																			
550	570	590																	
ATGTTCTGGCGACCCGTACTTCGCGCTGCCGCTCTTGGAATTGCTCCTGTGCGCCGAA																			
M	F	L	A	T	L	Y	F	A	L	P	L	L	D	L	L	L	S	A	E



## FIG.1D

610	630	650
GTGAGCGCGGAGACCGCCTGGATTGCCGTGAAAGCCAGTGATCAGTGCCCTGAAGGAGCAG		
V S G G D R L D C V K A S D Q C L K E Q		
670	690	710
AGCTGCAGCACCAAGTACCGCACGCTAAGGCAGTGCGTGGCGGGCAAGGAGACCAACTTC		
S C S T K Y R T L R Q C V A G K E T N F		
730	750	770
AGCCTGGCATCCGGCCTGGAGGCCCAAGGATGAGTGCCCGCAGCGCCCATGGAGGCCCTGAAG		
S L A S G L E A K D E C R S A M E A L K		



## FIG.1E

790	810	830
CAGAACTCGCTCTACAACCTGCCGCTGCAAGCGGGGTATGAAGAAGGAGAACTGCCCTG		
Q K S L Y N C R C K K R G M K K E K N C L		
850	870	890
CGCATTTACTGGAGCATGTACCCAGAGCCTGCAGGAAATGATCTGCTGGAGGATTCCCCA		
R I Y W S M Y Q S L Q G N D L L E D S P		
910	930	950
TATGAACCAGTTAACAGCAGATTGTCAGATATATTCGGGTGTCCTCATATCAGAT		
Y E P V N S R L S D I F R V V P F I S D		



# FIG.1F

970	990	1010
GTTTTTCAGCAAGTGGAGCACATTTCCCAAGGGAACAACCTGCCTGGATGCAGCGAAGGCC		
V F Q Q V E H I P K G N N C L D A A K A		
1030	1050	1070
TGCAACCTCGACGACATTTGCAAGAAGTACAGGTCGGCGGTACATCACCCCGTGCACCACC		
C N L D D I C K K Y R S A Y I T P C T T		
1090	1110	1130
AGCGTGTCCAACGATGCTGTCAACCGCCGCAAGTGCCACAAGGCCCTCCGGCAGTTCTTT		
S V S N D V C N R R K C H K A L R Q F F		



## FIG.1G

1150	1170	1190
GACAAGGTCCCGCCAAGCACAGCTACGGAATGCTCTTCTGCTCCTGCCGGACATCGCC		
D K V P A K H S Y G M L F C S C R D I A		
1210	1230	1250
TGCACAGCGGAGCGACAGACCATCGTGCCCTGTGTGCTCCTATGAAGAGAGGAGAAG		
C T E R R R Q T I V P V C S Y E E R E K		
1270	1290	1310
CCCAACTGTTGAATTTCAGGACTCCTGCAAGACGAATTACATCTGCAGATCTCGCCTT		
P N C L N L Q D S C K T N Y I C R S R L		





## FIG.1H

1330	1350	1370
GCGGATTTTACCAACTGCCAGCCAGAGTCAAGGCTGTCTCAGCAGCTGTCTAAAGGAA		
A D F F T N C Q P E S R S V S S C L K E		
1390	1410	1430
AACTACGCTGACTGCCCTCGCCTACTCGGGGCTTATTGGCACAGTCATGACCCCAAC		
N Y A D C L L A Y S G L I G T V M T P N		
1450	1470	1490
TACATAGACTCCAGTAGCCTCAGTGTGGCCCCCATGGTGTGACTGCAGCAACAGTGGGAAC		
Y I D S S S L S V A P W C D C S N S G N		

# FIG.1I

1510 1530 1550  
GACCTAGAAGAGTGCTTGAAATTTTGAATTCTTCAAGGACAAATACATGTCTTAAAAAT  
D L E E C L K F L N F F K D N T C L K N

1570 1590 1610  
GCAATTCAAGCCCTTTGGCAATGGCTCCGATGTGACCGTGTGGCAGCCAGCCTTCCCAGTA  
A I Q A F G N G S D V T V W Q P A F P V

1630 1650 1670  
CAGACCACCTGCCACTACCACCACTGCCCTCCGGTTAAGAACAAAGCCCCCTGGGGCCA  
Q T T A T T T A L R V K N K P L G P





## FIG.1J

1690	1710	1730
GCAGGGTCTGAGAAATGCCACTCATGTTTGGCCACCGTGCGCAAATTACAGGCA		
A G S E N E I P T H V L P P C A N L Q A		
1750	1770	1790
CAGAAAGCTGAAATCCAATGTGTCGGGCAATACACACCTCTGTATTTCCCAATGGTAATTAT		
Q K L K S N V S G N T H L C I S N G N Y		
1810	1830	1850
GAAAGAAAGGTCTCGGTGCTTCCAGCCACATACCAACAAATCAATGGCTGCTCCTCCA		
E K E G L G A S S H I T T K S M A A P P		



FIG. 1K

1870	1890	1910
AGCTGTGGTCTGAGCCCACTGCTGGTCCTGGTGGTAACCGCTCTGTGCCACCCCTATTATCT		
S C G L S P L L V L V T A L S T L L S		
1930	1950	1970
TTAACAGAAACATCATAGCTGCATTAAAAAATACAATATGGACATGTAAAAAGACAAAA		
L T E T S *		
1990	2010	2030
ACCAAGTTATCTGTTTCCCTGTTCTCTTGATAGCTGAAATTCCAGTTTAGGAGCTCAGTT		
2050	2070	2090
GAGAAACAGTTCATTCAACTGGAACATTTTTTTTTTTT.CCTTTTAAGAAAGCTTCTTGT		



## FIG.1L

2110	2130	2150
GATCCTT.GGGGCTTCTGTGAAAACCTGATGCAGTGCTCCATCCAAACTCAGAAGGCTT		
2170	2190	2210
TGGGATATGCTGTATTTTAAAGGGACAGTTTGTAAC TTGGGCTGTAAAGCAAAC TGGGGC		
2230	2250	2270
TG TGTTTTCGATGATGATGAT.ATCATGAT.ATGAT.....		
2290	2310	2330
.....GATTTTAAACAGTTT TACTTCTGGCCTTTCCTAGCTAGAGAAGGAG		



# FIG. 1M

2350	2370	2390
TTAATAATTTCTAAGGTAAGTCCCATATCTCCTTTTAATGACATTGATTTCTAATGATATAA		
2410	2430	2450
ATTTCAGCCTACATTGATGCCAAGCTTTTTTGGCCACAAGAAGATTCTTACCAAGAGTGG		
2470	2490	2510
GCTTTGTGGAAACAGCTGGTACTGATGTTTCACCTTTATATATGTACTAGCATTTTCCACG		
2530	2550	
CTGATGTTTATGTACTGTAAACAGTTCTGCACTCTTGTACAAAGAAA		



## FIG.2A

### Human Glial Cell Line-Derived Neurotrophic Factor Receptor Protein

M	F	L	A	T	L	Y	F	A	L	P	L	L	D	L	L	L	S	A	E	20
V	S	G	G	D	R	L	D	C	V	K	A	S	D	Q	C	L	K	E	Q	40
S	C	S	T	K	Y	R	T	L	R	Q	C	V	A	G	K	E	T	N	F	60
S	L	A	S	G	L	E	A	K	D	E	C	R	S	A	M	E	A	L	K	80
Q	K	S	L	Y	N	C	R	C	K	R	G	M	K	K	E	K	N	C	L	100
R	I	Y	W	S	M	Y	Q	S	L	Q	G	N	D	L	L	E	D	S	P	120
Y	E	P	V	N	S	R	L	S	D	I	F	R	V	V	P	F	I	S	D	140
V	F	Q	Q	V	E	H	I	P	K	G	N	N	C	L	D	A	A	K	A	160
C	N	L	D	D	I	C	K	K	Y	R	S	A	Y	I	T	P	C	T	T	180
S	V	S	N	D	V	C	N	R	R	K	C	H	K	A	L	R	Q	F	F	200
D	K	V	P	A	K	H	S	Y	G	M	L	F	C	S	C	R	D	I	A	220



FIG.2B

C	T	E	R	R	Q	T	I	V	P	V	C	S	Y	E	E	R	E	K	240
P	N	C	L	N	Q	D	S	C	K	T	N	Y	I	C	R	S	R	L	260
A	D	F	F	T	N	C	Q	P	E	S	R	S	V	S	C	L	K	E	280
N	Y	A	D	C	L	L	A	Y	S	G	L	I	G	T	V	M	T	P	300
Y	I	D	S	S	L	S	V	A	P	W	C	D	C	S	N	S	G	N	320
D	L	E	E	C	L	K	F	L	N	F	F	K	D	N	T	C	L	K	340
A	I	Q	A	F	G	N	G	S	D	V	T	V	W	Q	P	A	F	P	360
Q	T	T	A	T	T	T	T	A	L	R	V	K	N	K	P	L	G	P	380
A	G	S	E	N	E	I	P	T	H	V	L	P	P	C	A	N	L	Q	400
Q	K	L	K	S	N	V	S	G	N	T	H	L	C	I	S	N	G	N	420
E	K	E	G	L	G	A	S	S	H	I	T	T	K	S	M	A	A	P	440
S	C	G	L	S	P	L	L	V	L	V	V	T	A	L	S	T	L	S	460
L	T	E	T	S	*														

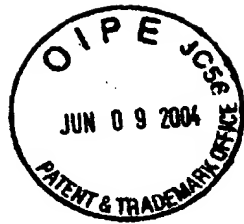




## FIG.3A

### Rat Glial Cell Line-Derived Neurotrophic Factor Receptor Protein

10	30	50
AGCTCGCTCTCCCGGGCAGTGGTGTGATGCACCGAGTTCGGGCGCTGGGCAAGTTGG		
70	90	110
GTCGGAACTGAACCCCTGAAAGCGGGTCCGCCCTCCCGCCCTCGCGCCCGCGGATCTGA		
130	150	170
GTCGCTGGCGGGTGGCGGCAGAGCGACGGGGAGTCTGCTCTCACCCCTGGATGGAGCT		



## FIG.3B

190	210	230
GAACTTTGAGTGGCCAGAGGAGCGCAGTCGCCCGGGGATCGCTGCACGCTGAGCTCTCTC		
250	270	290
CCCGAGACCGGGCGGGCTTTGGATTTTGGGGGGGGGACCAGCTGCGCGGGGCAC		
310	330	350
CATGTTCCCTAGCCACTCTGTACTTCGCGCTGCCACTCCTGGATTGCTGATGTCCGCCGA		
M F L A T L Y F A L P L L D L L M S A E		
370	390	410
GGTGAGTGGTGAGACCGTCTGGACTGTGTGAAAGCCAGCGATCAGTGCCCTGAAGGAACA		
V S G G D R L D C V K A S D Q C L K E Q		



## FIG.3C

430	450	470
GAGCTGCAGCACCAAGTACCGCACACTAAGGCAGTGCGTGGCGGCAAGGAAACCAACTT		
S	C	T
K	Y	R
T	L	R
Q	C	V
A	G	K
E	T	N
F		
490	510	530
CAGCCTGACATCCGGCCTTGAGGCCCAAGGATGAGTGCCGTAGCGCCATGGAGGCCTTGAA		
S	L	T
S	G	L
E	A	K
D	E	C
R	S	A
M	E	A
L	K	



## FIG.3D

550	570	590																	
GCAGAACTCTGTACAAGTCCGCTGCAAGCGGGGCATGAAGAAAGAGAAGAAATTGTCT																			
Q	K	S	L	Y	N	C	R	C	K	R	G	M	K	K	E	K	N	C	L
610			630	650															
GCGTATCTACTGGAGCATGTACCAGAGCCTGCAGGGAAATGACCTCCTGGAAGATTCCCC																			
R	I	Y	W	S	M	Y	Q	S	L	Q	G	N	D	L	L	E	D	S	P
670			690	710															
GTATGAGCCGGTTAACAGCAGGTTGTCAGATATATCCGGGCAGTCCCGTTTCATATCAGA																			
Y	E	P	V	N	S	R	L	S	D	I	F	R	A	V	P	F	I	S	D



## FIG.3E

730	750	770
TGTTTCCAGCAAGTGGAAACACATTTCCAAAGGGAACAACCTGGACGCAGCCAAGGC		
V F Q Q V E H I S K G N N C L D A A K A		
790	810	830
CTGCAACCTGGACGACACCTGTAAAGAAGTACAGGTCGGCCTACATCACCCCTGCACCAC		
C N L D D T C K K Y R S A Y I T P C T T		
850	870	890
CAGCATGTCCAACGAGGTCTGCAACCGCCGTAAGTGCCACAAGGCCCTCAGGCAGTTCTT		
S M S N E V C N R R K C H K A L R Q F F		



## FIG.3F

910	930	950
CGACAAGGTTCCGGCCAAGCACAGCTACGGGATGCTCTTCTGCTCCTGCCGGGACATCGC		
D K V P A K H S Y G M L F C S C R D I A		
970	990	1010
CTGCACCGAGCGGCGACAGACTATCGTCCCCGTGTGCTCCTATGAAGAACGAGAGAG		
C T E R R R Q T I V P V C S Y E E R E R		
1030	1050	1070
GCCCAACTGCCCTGAGTCTGCAAGACTCCTGCAAGACCAATTACATCTGCAGATCTCGCCT		
P N C L S L Q D S C K T N Y I C R S R L		



## FIG.3G

1090	1110	1130
TGCAGATTTTACCAACTGCCAGCCAGAGTCAAGGCTGTCTCAGCAACTGTCTTAAGGA		
A D F F T N C Q P E S R S V S N C L K E		
1150	1170	1190
GAACTACGCAGACTGCCCTCCTGGCCTACTCGGGACTGATTGGCACAGTCATGACTCCCAA		
N Y A D C L L A Y S G L I G T V M T P N		
1210	1230	1250
CTACGTAGACTCCAGCAGCCCTCAGCGTGGCACCATGGTGTGACTGCCAGCAACAGCGGCAA		
Y V D S S S L S V A P W C D C S N S G N		



## FIG.3H

1270	1290	1310
TGACCTGGAAGACTGCTTGAAATTCTCTGAATTTTTTAAGGACAAATACTTGTCTCAAAA		
D L E D C L K F L N F F K D N T C L K N		
1330	1350	1370
TGCAATTCAAGCCTTTGGCAATGGCTCAGATGTGACCATGTGGCAGCCAGCCCCCTCCAGT		
A I Q A F G N G S D V T M W Q P A P P V		
1390	1410	1430
CCAGACCACCACTGCCACCACTACCACTGCCCTTCCGGGTCAAGAACAGCCTCTGGGGCC		
Q T T T A T T T A F R V K N K P L G P		





## FIG.3I

1450	1470	1490
AGCAGGGTCTGAGAA	TGAGATCCCCACACACGTTT	TACCACCCCTGTGCGAATTTCAGGC
A G S E N E I P T H V L P P C A N L Q A		
1510	1530	1550
TCAGAAGCTGAAATCCAATGTGTCGGGTAGCACACACCTCTGTCTTTCTGATAGTGATTT		
Q K L K S N V S G S T H L C L S D S D F		
1570	1590	1610
CGGAAAGGATGGTCTCGCTGGTGCCTCCAGCCACATAACCCACAAAATCAATGGCTGCTCC		
G K D G L A G A S S H I T T K S M A A P		

FIG.3J

1630	1650	1670
TCCAGCTGCAGTCTGAGCTCACTGCCGGTGCTGATGCTCACCGCCCTTGCTGCCCTGTT		
P S C S L S S L P V L M L T A L A L L		
1690	1710	1730
ATCTGTATCGTTGGCAGAAACGTCGTAGCTGCATCCGGGAAACAGTATGAAAGACAAA		
S V S L A E T S *		
1750	1770	1790
AGAGAACCAAGTATTCTGTCCCCTGTCCCTCTTGTTATATCTGAAAATCCAGTTTAAAGCT		
1810	1830	1850
CCGTTGAGAAGCAGTTTCACCCCAACTGGAACCTTTCCTTGTTTAAAGAAAGCTTGTTGG		





## FIG.3K

1870	1890	1910
CCCTCAGGGCTTCTGTGAAGAACTGCTACAGGGCTAATTCCAAACCCATAAGGCTCTG		
1930	1950	1970
GGCGTGGTGCGGCTTAAGGGACCATTTCACCATGTAAAGCAAGCTGGGCTTATCATG		
1990	2010	2030
TGTTTGATGGTGAGGATGGTAGTGGTGATGATGGTAATTTAAACAGCTTGAACCCCTG		
2050	2070	2090
TTCTCTCTACTGGTTAGGAACAGGAGATACTATTGATAAAGATTCTTCCATGTCTTACTC		
2110	2130	
AGCAGCATTGCCTTCTGAAGACAGGCCCGCAGCCGTCG		



## FIG.4A

### Rat Glial Cell Line-Derived Neurotrophic Factor Receptor Protein

M	F	L	A	T	L	Y	F	A	L	P	L	L	D	L	L	M	S	A	E	20
V	S	G	G	D	R	L	D	C	V	K	A	S	D	Q	C	L	K	E	Q	40
S	C	S	T	K	Y	R	T	L	R	Q	C	V	A	G	K	E	T	N	F	60
S	L	T	S	G	L	E	A	K	D	E	C	R	S	A	M	E	A	L	K	80
Q	K	S	L	Y	N	C	R	C	K	R	G	M	K	K	E	K	N	C	L	100
R	I	Y	W	S	M	Y	Q	S	L	Q	G	N	D	L	L	E	D	S	P	120
Y	E	P	V	N	S	R	L	S	D	I	F	R	A	V	P	F	I	S	D	140
V	F	Q	Q	V	E	H	I	S	K	G	N	N	C	L	D	A	A	K	A	160
C	N	L	D	D	T	C	K	K	Y	R	S	A	Y	I	T	P	C	T	T	180
S	M	S	N	E	V	C	N	R	R	K	C	H	K	A	L	R	Q	F	F	200
D	K	V	P	A	K	H	S	Y	G	M	L	F	C	S	C	R	D	I	A	220
C	T	E	R	R	Q	T	I	V	P	V	C	S	Y	E	R	E	R	E	R	240



FIG.4B

P	N	C	L	S	L	Q	D	S	C	K	T	N	Y	I	C	R	S	R	L	260
A	D	F	F	T	N	C	Q	P	E	S	R	S	V	S	N	C	L	K	E	280
N	Y	A	D	C	L	L	A	Y	S	G	L	I	G	T	V	M	T	P	N	300
Y	V	D	S	S	S	L	S	V	A	P	W	C	D	C	S	N	S	G	N	320
D	L	E	D	C	L	K	F	L	N	F	F	K	D	N	T	C	L	K	N	340
A	I	Q	A	F	G	N	G	S	D	V	T	M	W	Q	P	A	P	P	V	360
Q	T	T	A	T	T	T	T	T	A	F	R	V	K	N	K	P	L	G	P	380
A	G	S	E	N	E	I	P	T	H	V	L	P	P	C	A	N	L	Q	A	400
Q	K	L	K	S	N	V	S	G	S	T	H	L	C	L	S	D	S	D	F	420
G	K	D	G	L	A	G	A	S	S	H	I	T	T	K	S	M	A	A	P	440
P	S	C	S	L	S	S	L	P	V	L	M	L	T	A	L	A	A	L	L	460
S	V	S	L	A	E	T	S	*												

**FIG. 5A**

Human GDNF receptor Clones -- Alignment to generate consensus sequence

(SEQ ID NO:45)	Gdnfr	AATCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACCTA
(SEQ ID NO:46)	Hsgr-21af	TCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACCTA
(SEQ ID NO:47)	Hsgr-21bf	AATCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACCTA
(SEQ ID NO:48)	21acon	TCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACCTA
(SEQ ID NO:49)	21bcon	AATCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACCTA

(SEQ ID NO:45)	Gdnfr	-187	-138
(SEQ ID NO:46)	Hsgr-21af	ACATCCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG	
(SEQ ID NO:47)	Hsgr-21bf	ACATCCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG	
(SEQ ID NO:48)	21acon	ACATCCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG	
(SEQ ID NO:49)	21bcon	ACATCCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG	

(SEQ ID NO:45)	Gdnfr	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA	TTACCGCATC	TATTTTTTTTTT
(SEQ ID NO:46)	Hsgr-21af	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA	TTACCGCATC	TATTTTTTTTTT
(SEQ ID NO:47)	Hsgr-21bf	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA	TTACCGCATC	TATTTTTTTTTT
(SEQ ID NO:48)	21acon	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA	TTACCGCATC	TATTTTTTTTTT
(SEQ ID NO:49)	21bcon	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA	TTACCGCATC	TATTTTTTTTTT



## FIG. 5C

(SEQ ID NO:45)		113				162
(SEQ ID NO:46)	Gdnfr	AGCTGAGTCG	CCGGCGGCGG	TGGCTGCTGC	CAGACCCGGA	GTTTCCCTCTT
(SEQ ID NO:47)	Hsgr-21af	AGCTGAGTCG	CCGGCGGCGG	TGGCTGCTGC	CAGACCCGGA	GTTTCCCTCTT
(SEQ ID NO:48)	Hsgr-21bf	AGCTGAGTCG	CCGGCGGCGG	TGGCTGCTGC	CAGACCCGGA	GTTTCCCTCTT
(SEQ ID NO:49)	21acon	AGCTGAGTCG	CCGGCGGCGG	TGGCTGCTGC	CAGACCCGGA	GTTTCCCTCTT
	21bcon	AGCTGAGTCG	CCGGCGGCGG	TGGCTGCTGC	CAGACCCGGA	GTTTCCCTCTT
(SEQ ID NO:45)		163				212
(SEQ ID NO:46)	Gdnfr	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC	AGAGCAGCAC	AGCTGTCCGG
(SEQ ID NO:47)	Hsgr-21af	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC	AGAGCAGCAC	AGCTGTCCGG
(SEQ ID NO:48)	Hsgr-21bf	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC	AGAGCAGCAC	AGCTGTCCGG
(SEQ ID NO:49)	21acon	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC	AGAGCAGCAC	AGCTGTCCGG
	21bcon	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC	AGAGCAGCAC	AGCTGTCCGG
(SEQ ID NO:45)		213				262
(SEQ ID NO:46)	Gdnfr	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA	GACCCAGCGG	CGGCTCGGGA
(SEQ ID NO:47)	Hsgr-21af	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA	GACCCAGCGG	CGGCTCGGGA
(SEQ ID NO:48)	Hsgr-21bf	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA	GACCCAGCGG	CGGCTCGGGA
(SEQ ID NO:49)	21acon	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA	GACCCAGCGG	CGGCTCGGGA
	21bcon	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA	GACCCAGCGG	CGGCTCGGGA
(SEQ ID NO:45)		263				312
(SEQ ID NO:46)	Gdnfr	TTTTTTTGGG	GGGGCGGGGA	CCAGCCCCCGC	GCCGGCACCA	TGTTCCCTGGC
(SEQ ID NO:47)	Hsgr-21af	TTTTTTTGGG				
(SEQ ID NO:48)	Hsgr-21bf	TTTTTTTGGG				
(SEQ ID NO:49)	21acon	TTTTTTTGGG	GGGGCGGGGA	CCAGCCCCCGC	GCCGGCACCA	TGTTCCCTGGC
	21bcon	TTTTTTTGGG	GGGGCGGGGA	CCAGCCCCCGC	GCCGGCACCA	TGTTCCCTGGC



# FIG. 5D

(SEQ ID NO:45)	Gdnfr	GACCCCTGTAC	TTCGCGCTGC	CGCTCTTGGA	CTTGCTCCTG	TCGGCCGAAG	362
(SEQ ID NO:48)	21acon	GNCCCTGTAC	TTCGCGCTGC	CGCTCTTGGA	CTTGCTCCTG	TCGGCCGAAG	
(SEQ ID NO:49)	21bcon	GACCCCTGTAC	TTCGCGCTGC	CGCTCTTGGA	CTTGCTCCTG	TCGGCCGAAG	
(SEQ ID NO:45)	Gdnfr	TGAGCGGCGG	AGACCGCCTG	GATTGCGTGA	AAGCCAGTGA	TCAGTGCCTG	412
(SEQ ID NO:48)	21acon	TGAGCGGCGG	AGACCGCCTG	GATTGCGTGA	AAGCCAGTGA	TCAGTGCCTG	
(SEQ ID NO:49)	21bcon	TGAGCGGCGG	AGACCGCCTG	GATTGCGTGA	AAGCCAGTGA	TCAGTGCCTG	
(SEQ ID NO:45)	Gdnfr	AAGGAGCAGA	GCTGCAGCAC	CAAGTACCGC	ACGCTAAGGC	AGTGCGTGGC	462
(SEQ ID NO:48)	21acon	AAGGAGCAGA	GCTGCAGCAC	CAAGTACCGC	ACGCTAAGGC	AGTGCGTGGC	
(SEQ ID NO:49)	21bcon	AAGGAGCAGA	GCTGCAGCAC	CAAGTACCGC	ACGCTAAGGC	AGTGCGTGGC	
(SEQ ID NO:45)	Gdnfr	GGGCAAGGAG	ACCAACTTCA	GCCTGGCATC	CGGCCTGGAG	GCCAAGGATG	512
(SEQ ID NO:48)	21acon	GGGCAAGGAG	ACCAACTTCA	GCCTGGCATC	CGGCCTGGAG	GCCAAGGATG	
(SEQ ID NO:49)	21bcon	GGGCAAGGAG	ACCAACTTCA	GCCTGGCATC	CGGCCTGGAG	GCCAAGGATG	
(SEQ ID NO:45)	Gdnfr	AGTGCCGCAG	CGCCATGGAG	GCCCTGAAGC	AGAAGTCGCT	CTACAACTGC	562
(SEQ ID NO:48)	21acon	AGTGCCGCAG	CGCCATGGAG	GCCCTGAAGC	AGAAGTCGCT	CTACAACTGC	
(SEQ ID NO:49)	21bcon	AGTGCCGCAG	CGCCATGGAG	GCCCTGAAGC	AGAAGTCGCT	CTACAACTGC	





## FIG. 5E

(SEQ ID NO: 45)	Gdnfr	563	612
(SEQ ID NO: 48)	21acon	CGCTGCAAGC GGGGTATGAA GAAAGAGAAG AACTGCCTGC GCATTTACTG	
(SEQ ID NO: 49)	21bcon	CGCTGCAAGC GGGGTATGAA GAAAGAGAAG AACTGCCTGC GCATTTACTG	
(SEQ ID NO: 45)	Gdnfr	663	662
(SEQ ID NO: 48)	21acon	GAGCATGTAC CAGAGCCTGC AGGGAATGA TCTGCTGGAG GATCCCCCAT	
(SEQ ID NO: 49)	21bcon	GAGCATGTAC CAGAGCCTGC AGGGAATGA TCTGCTGGAG GATCCCCCAT	
(SEQ ID NO: 45)	Gdnfr	663	712
(SEQ ID NO: 48)	21acon	ATGAACCAGT TAACAGCAGA TTGTCAGATA TATCCCGGT GGTCCCATTC	
(SEQ ID NO: 49)	21bcon	ATGAACCAGT TAACAGCAGA TTGTCAGATA TATCCCGGT GGTCCCATTC	
(SEQ ID NO: 45)	Gdnfr	713	762
(SEQ ID NO: 48)	21acon	ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACTG	
(SEQ ID NO: 49)	21bcon	ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACTG	
(SEQ ID NO: 45)	Gdnfr	763	812
(SEQ ID NO: 48)	21acon	CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTTC AAGAAGTACA	
(SEQ ID NO: 49)	21bcon	CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTTC AAGAAGTACA	

## FIG. 5F

		813	862
(SEQ ID NO:45)	Gdnfr	GGTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA .GATGTCCTGC	
(SEQ ID NO:50)	Hsgr-29a	GTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA TGATGTCCTGC	
(SEQ ID NO:48)	21acon	GGTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA CGATGTCCTGC	
(SEQ ID NO:49)	21bcon	GGTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA CGATGTCCTGC	
(SEQ ID NO:51)	29brc	GTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA TGATGTCCTGC	

(SEQ ID NO: 45)	Gdnfr	863	912
(SEQ ID NO: 50)	Hsgr-29a	AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC	
(SEQ ID NO: 48)	21acon	AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC	
(SEQ ID NO: 49)	21bcon	AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC	
(SEQ ID NO: 51)	29brc	AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC	

		913	962
(SEQ ID NO:45)	Gdnfr	GGCCAAGCAC AGCTACGGAA TGCTCTTCTG	CTCCTGCCGG GACATCGCCT
(SEQ ID NO:50)	Hsgr-29a	GGCCAAGCAC AGCTACGGAA TGCTCTTCTG	CTCCTGCCGG GACATCGCCT
(SEQ ID NO:48)	21acon	GGCCAAGCAC AGCTACGGAA TGCTCTTCTG	CTCCTGCCGG GACATCGCCT
(SEQ ID NO:49)	21bcon	GGCCAAGCAC AGCTACGGAA TGCTCTTCTG	CTCCTGCCGG GACATCGCCT
(SEQ ID NO:51)	29brc	GGCCAAGCAC AGCTACGGAA TGCTCTTCTG	CTCCTGCCGG GACATCGCCT

		963	1012
(SEQ ID NO:45)	Gdnfr	GCACAGAGCG GAGCGACAG ACCATCGTGC	CTGTGTGCTC CTATGAAGAG
(SEQ ID NO:50)	Hsgr-29a	GCACAGAGCG GAGCGACAG ACCATCGTGC	CTGTGTGCTC CTATGAAGAG
(SEQ ID NO:48)	21acon	GCACAGAGCG GAGCGACAG ACCATCGTGC	CTGTGTGCTC CTATGAAGAG
(SEQ ID NO:49)	21bcon	GCACAGAGCG GAGCGACAG ACCATCGTGC	CTGTGTGCTC CTATGAAGAG
(SEQ ID NO:51)	29brc	GCACAGAGCG GAGCGACAG ACCATCGTGC	CTGTGTGCTC CTATGAAGAG

## FIG. 5G

		1013		1062
(SEQ ID NO: 45)	Gdnfr	AGGGAGAAGC CCAACTGTTT	GAAATTGCAG	GACTCCTGCA AGACGAATTA
(SEQ ID NO: 52)	Hsgr-21ar		GAAATTGCAG	GACTCCTGCA AGACGAATTA
(SEQ ID NO: 53)	Hsgr-21br			A
(SEQ ID NO: 50)	Hsgr-29a	AGGGAGAAGC CCAACTGTTT	GAAATTGCAG	GACTCCTGCA AGACGAATTA
(SEQ ID NO: 48)	21acon	AGGGAGAAGC CCAACTGTTT	GAAATTGCAG	GACTCCTGCA AGACGAATTA
(SEQ ID NO: 49)	21bcon	AGGGAGAAGC CCAACTGTTT	GAAATTGCAG	GACTCCTGCA AGACGAATTA
(SEQ ID NO: 51)	29brc	AGGGAGAAGC CCAACTGTTT	GAAATTGCAG	GACTCCTGCA AGACGAATTA
		1063		1112
(SEQ ID NO: 45)	Gdnfr	CATCTGCAGA TCTCGCCTTG	CGGATTTTTT	TACCAACTGC CAGCCAGAGT
(SEQ ID NO: 52)	Hsgr-21ar	CATCTGCAGA TCTCGCCTTG	CGGATTTTTT	TACCAACTGC CAGCCAGAGT
(SEQ ID NO: 53)	Hsgr-21br	CATCTGCAGA TCTCGCCTTG	CGGATTTTTT	TACCAACTGC CAGCCAGAGT
(SEQ ID NO: 50)	Hsgr-29a	CATCTGCAGA TCTCGCCTTG	CGGATTTTTT	TACCAACTGC CAGCCAGAGT
(SEQ ID NO: 48)	21acon	CATCTGCAGA TCTCGCCTTG	CGGATTTTTT	TACCAACTGC CAGCCAGAGT
(SEQ ID NO: 49)	21bcon	CATCTGCAGA TCTCGCCTTG	CGGATTTTTT	TACCAACTGC CAGCCAGAGT
(SEQ ID NO: 51)	29brc	CATCTGCAGA TCTCGCCTTG	CGGATTTTTT	TACCAACTGC CAGCCAGAGT
		1113		1162
(SEQ ID NO: 45)	Gdnfr	CAAGGTCTGT CAGCAGCTGT	CTAAAGGAAA	ACTACGCTGA CTGCCTCCTC
(SEQ ID NO: 52)	Hsgr-21ar	CAAGGTCTGT CAGCAGCTGT	CTAAAGGAAA	ACTACGCTGA CTGCCTCCTC
(SEQ ID NO: 53)	Hsgr-21br	CAAGGTCTGT CAGCAGCTGT	CTAAAGGAAA	ACTACGCTGA CTGCCTCCTC
(SEQ ID NO: 50)	Hsgr-29a	CAAGGTCTGT CAGCAGCTGT	CTAAAGGAAA	ACTACGCTGA CTGCCTCCTC
(SEQ ID NO: 48)	21acon	CAAGGTCTGT CAGCAGCTGT	CTAAAGGAAA	ACTACGCTGA CTGCCTCCTC
(SEQ ID NO: 49)	21bcon	CAAGGTCTGT CAGCAGCTGT	CTAAAGGAAA	ACTACGCTGA CTGCCTCCTC
(SEQ ID NO: 51)	29brc	CAAGGTCTGT CAGCAGCTGT	CTAAAGGAAA	ACTACGCTGA CTGCCTCCTC



## FIG. 5H

(SEQ ID NO:45)		1163				1212
(SEQ ID NO:52)	Gdnfr	GCCTACTCGG	GGCTTATTGG	CACAGTCATG	ACCCCCAACT	ACATAGACTC
(SEQ ID NO:53)	Hsgr-21ar	GCCTACTCGG	GGCTTATTGG	CACAGTCATG	ACCCCCAACT	ACATAGACTC
(SEQ ID NO:50)	Hsgr-21br	GCCTACTCGG	GGCTTATTGG	CACAGTCATG	ACCCCCAACT	ACATAGACTC
(SEQ ID NO:48)	Hsgr-29a	GCCTACTCGG	GGCTTATTGG	CACAGTCATG	ACCCCCAACT	ACATAGACTC
(SEQ ID NO:49)	21acon	GCCTACTCGG	GGCTTATTGG	CACAGTCATG	ACCCCCAACT	ACATAGACTC
(SEQ ID NO:51)	21bcon	GCCTACTCGG	GGCTTATTGG	CACAGTCATG	ACCCCCAACT	ACATAGACTC
	29brc	GCCTACTCGG	GGCTTATTGG	CACAGTCATG	ACCCCCAACT	ACATAGACTC
(SEQ ID NO:45)		1213				1262
(SEQ ID NO:54)	Gdnfr	CAGTAGCCTC	AGTGTGGCCC	CATGGTGTGA	CTGCAGCAAC	AGTGGGAACG
(SEQ ID NO:52)	Hsgr-2					TGGGAACG
(SEQ ID NO:53)	Hsgr-21ar	CAGTAGCCTC	AGTGTGGCCC	CATGGTGTGA	CTGCAGCAAC	AGTGGGAACG
(SEQ ID NO:50)	Hsgr-21br	CAGTAGCCTC	AGTGTGGCCC	CATGGTGTGA	CTGCAGCAAC	AGTGGGAACG
(SEQ ID NO:48)	Hsgr-29a	CAGTAGCCTC	AGTGTGGCCC	CATGGTGTGA	CTGCAGCAAC	AGTGGGAACG
(SEQ ID NO:49)	21acon	CAGTAGCCTC	AGTGTGGCCC	CATGGTGTGA	CTGCAGCAAC	AGTGGGAACG
(SEQ ID NO:51)	21bcon	CAGTAGCCTC	AGTGTGGCCC	CATGGTGTGA	CTGCAGCAAC	AGTGGGAACG
	29brc	CAGTAGCCTC	AGTGTGGCCC	CATGGTGTGA	CTGCAGCAAC	AGTGGGAACG

# FIG. 5I

(SEQ ID NO:45)		1263			1312
(SEQ ID NO:54)	Gdnfr	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA
(SEQ ID NO:55)	Hsgr-2	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA
(SEQ ID NO:52)	Hsgr-9		A	TTTTTGAATT	TCTTCAAGGA
(SEQ ID NO:53)	Hsgr-21ar	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA
(SEQ ID NO:50)	Hsgr-21br	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA
(SEQ ID NO:48)	Hsgr-29a	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA
(SEQ ID NO:49)	21acon	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA
(SEQ ID NO:51)	21bcon	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA
	29brc	ACCTAGAAGA	GTGCTTGAAA	TTTTTGAATT	TCTTCAAGGA

(SEQ ID NO:45)		1313			1362
(SEQ ID NO:54)	Gdnfr	CTTAAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG
(SEQ ID NO:55)	Hsgr-2	CTTAAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG
(SEQ ID NO:52)	Hsgr-9	CTTAAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG
(SEQ ID NO:53)	Hsgr-21ar	CTTAAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG
(SEQ ID NO:50)	Hsgr-21br	CTTAAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG
(SEQ ID NO:48)	Hsgr-29a	CTTAAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG
(SEQ ID NO:49)	21acon	CTTAAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG
(SEQ ID NO:51)	21bcon	CTTAAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG
	29brc	CTTAAAAAATG	CAATTCAAGC	CTTTGGCAAT	GGCTCCGATG



FIG. 5J

			1363				1412
(SEQ ID NO: 45)	Gdnfr	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCaCTACC	ACCACTGCCC	
(SEQ ID NO: 54)	Hsgr-2	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCACTACC	ACCACTGCCC	
(SEQ ID NO: 55)	Hsgr-9	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCACTACC	ACCACTGCCC	
(SEQ ID NO: 52)	Hsgr-21ar	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCACTACC	ACCACTGCCC	
(SEQ ID NO: 53)	Hsgr-21br	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCACTACC	ACCACTGCCC	
(SEQ ID NO: 50)	Hsgr-29a	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCGCTACC	ACCACTGCCC	
(SEQ ID NO: 48)	21acon	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCACTACC	ACCACTGCCC	
(SEQ ID NO: 49)	21bcon	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCACTACC	ACCACTGCCC	
(SEQ ID NO: 51)	29brc	GCAGCCAGCC	TTCCCAGTAC	AGACCACCAC	TGCCGCTACC	ACCACTGCCC	
			1413				1462
(SEQ ID NO: 45)	Gdnfr	TCCGGGTTAA	GAACAAGCCC	CTGGGGCCAG	CAGGGTCTGA	GAATGAAATT	
(SEQ ID NO: 54)	Hsgr-2	TCCGGGTTAA	GAACAAGCCC	CTGGGGCCAG	CAGGGTCTGA	GAATGAAATT	
(SEQ ID NO: 55)	Hsgr-9	TCCGGGTTAA	GAACAAGCCC	CTGGGGCCAG	CAGGGTCTGA	GAATGAAATT	
(SEQ ID NO: 52)	Hsgr-21ar	TCCGGGTTAA	GAACAAGCCC	CTGGGGCCAG	CAGGGTCTGA	GAATGAAATT	
(SEQ ID NO: 53)	Hsgr-21br	TCCGGGTTAA	GAACAAGCCC	CTGGGGCCAG	CAGGGTCTGA	GAATGAAATT	
(SEQ ID NO: 50)	Hsgr-29a	TCCGGGTTAA	GAACAAGCCC	CTGGGGCCAG	CAGGGTCTGA	GAATGAAATT	
(SEQ ID NO: 48)	21acon	TCCGGGTTAA	GAACAAGCCC	CTGGGGCCAG	CAGGGTCTGA	GAATGAAATT	
(SEQ ID NO: 49)	21bcon	TCCGGGTTAA	GAACAAGCCC	CTGGGGCCAG	CAGGGTCTGA	GAATGAAATT	
(SEQ ID NO: 51)	29brc	TCCGGGTTAA	GAACAAGCCC	CTGGGGCCAG	CAGGGTCTGA	GAATGAAATT	



				1513		1562
(SEQ ID NO: 45)	Gdnfr	ATCCAAATGTG	TCGGGCAATA	CACACCTCTG	TATTTCCAAT	GGTAATTATG
(SEQ ID NO: 54)	Hsgr-2	ATCCAAATGTG	TCGGGCAATA	CACACCTCTG	TATTTCCAAT	GGTAATTATG
(SEQ ID NO: 55)	Hsgr-9	ATCCAAATGTG	TCGGGCAATA	CACACCTCTG	TATTTCCAAT	GGTAATTATG
(SEQ ID NO: 52)	Hsgr-21ar	ATCCAAATGTG	TCGGGCAATA	CACACCTCTG	TATTTCCAAT	GGTAATTATG
(SEQ ID NO: 53)	Hsgr-21br	ATCCAAATGTG	TCGGGCAATA	CACACCTCTG	TATTTCCAAT	GGTAATTATG
(SEQ ID NO: 48)	21acon	ATCCAAATGTG	TCGGGCAATA	CACACCTCTG	TATTTCCAAT	GGTAATTATG
(SEQ ID NO: 49)	21bcon	ATCCAAATGTG	TCGGGCAATA	CACACCTCTG	TATTTCCAAT	GGTAATTATG
(SEQ ID NO: 51)	29brc	ATCCAAATGTG	TCGGGCAATA	CACACCTCTG	TATTTCCAAT	GGTAATTATG





## FIG. 5L

(SEQ ID NO:45)		1563				1612
(SEQ ID NO:54)	Gdnfr	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAAACCACAAA	ATCAATGGCT
(SEQ ID NO:55)	Hsgr-2	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAAACCACAAA	ATCAATGGCT
	Hsgr-9	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAAACCACAAA	ATCAATGGCT
	Hsgr-21ar	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAAACCACAAA	ATCAATGGCT
(SEQ ID NO:53)	Hsgr-21br	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAAACCACAAA	ATCAATGGCT
(SEQ ID NO:48)	21acon	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAAACCACAAA	ATCAATGGCT
(SEQ ID NO:49)	21bcon	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAAACCACAAA	ATCAATGGCT
(SEQ ID NO:51)	29brc	AAAAAGAAGG	TCTCGGTGCT	TCCAGCCACA	TAAACCACAAA	ATCAATGGCT
(SEQ ID NO:45)		1613				1662
(SEQ ID NO:54)	Gdnfr	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCCG
(SEQ ID NO:55)	Hsgr-2	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCCG
	Hsgr-9	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCCG
	Hsgr-21ar	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCCG
(SEQ ID NO:53)	Hsgr-21br	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCCG
(SEQ ID NO:48)	21acon	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCCG
(SEQ ID NO:49)	21bcon	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCCG
(SEQ ID NO:51)	29brc	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG	CTGGTCCTGG	TGGTAACCCG

# FIG. 5M

(SEQ ID NO:45)	Gdnfr	1663	1712
(SEQ ID NO:54)	Hsgr-2	TCTGTCCACC CTATTATCTT	TAAACAGAAAC ATCATAGCTG CATTAAGAAA
(SEQ ID NO:55)	Hsgr-9	TCTGTCCACC CTATTATCTT	TAAACAGAAAC ATCATAGCTG CATTAAGAAA
(SEQ ID NO:52)	Hsgr-21ar	TCTGTCCACC CTATTATCTT	TAAACAGAAA
(SEQ ID NO:53)	Hsgr-21br	TCTGTCCACC CTATTATCTT	TAAACAGAAA
(SEQ ID NO:48)	21acon	TCTGTCCACC CTATTATCTT	TAAACAGAAA
(SEQ ID NO:49)	21bcon	TCTGTCCACC CTATTATCTT	TAAACAGAAA
(SEQ ID NO:51)	29brc	TCTGTCCACC CTATTATCTT	TAAACAGAAAC ATCATAGCTG CATTAAGAAA
(SEQ ID NO:45)	Gdnfr	1713	1762
(SEQ ID NO:54)	Hsgr-2	ATACAAATATG GACATGTAAA	AAGACAAAAA CCAAGTTATC TGTTTCCTGT
(SEQ ID NO:55)	Hsgr-9	ATACAAATATG GACATGTAAA	AAGACAAAAA CCAAGTTATC TGTTTCCTGT
(SEQ ID NO:51)	29brc	ATACAAATATG GACATGTAAA	AAGACAAAAA CCAAGTTATC TGTTTCCTGT
(SEQ ID NO:45)	Gdnfr	1763	1812
(SEQ ID NO:54)	Hsgr-2	TCTCTTGTAT AGCTGAAATT	CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
(SEQ ID NO:55)	Hsgr-9	TCTCTTGTAT AGCTGAAATT	CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
(SEQ ID NO:51)	29brc	TCTCTTGTAT AGCTGAAATT	CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
(SEQ ID NO:45)	Gdnfr	1813	1862
(SEQ ID NO:54)	Hsgr-2	CCATTCAACT GGAACATTTT	TTTTTTT.CC TTTTAAGAAA GCTTCTTG TG
(SEQ ID NO:55)	Hsgr-9	CCATTCAACT GGAACATTTT	TTTTTTT.CC TTTTAAGAAA GCTTCTTG TG
(SEQ ID NO:51)	29brc	CCATTCAACT GGAACATTTT	TTTTTTT.CC TTTTAAGAAA GCTTCTTG TG



## FIG. 5N

(SEQ ID NO:45)		1863		1912
	Gdnfr	ATCCTTCGGG	GCTTCTGTGA	AAAACCTGAT
(SEQ ID NO:54)	Hsgr-2	ATCCTTCGGG	GCTTCTGTGA	AAAACCTGAT
(SEQ ID NO:55)	Hsgr-9	ATCCTTCGGG	GCTTCTGTGA	AAAACCTGAT
(SEQ ID NO:51)	29brc	ATCCTTCGGG	GCTTCTGTGA	AAAACCTGAT
				1962
(SEQ ID NO:45)	Gdnfr	AGAAGGCTTT	GGGATATGCT	GTATTTTAAA
(SEQ ID NO:54)	Hsgr-2	AGAAGGCTTT	GGGATATGCT	GTATTTTAAA
(SEQ ID NO:55)	Hsgr-9	AGAAGGCTTT	GGGATATGCT	GTATTTTAAA
(SEQ ID NO:51)	29brc	AGAAGGCTTT	GGGATATGCT	GTATTTTAAA
				2012
(SEQ ID NO:45)	Gdnfr	CTGTAAAGCA	AACTGGGGCT	GTGTTTTCGA
(SEQ ID NO:54)	Hsgr-2	CTGTAAAGCA	AACTGGGGCT	GTGTTTTCGA
(SEQ ID NO:55)	Hsgr-9	CTGTAAAGCA	AACTGGGGCT	GTGTTTTCGA
(SEQ ID NO:51)	29brc	CTGTAAAGCA	AACTGGGGCT	GTGTTTTCGA
				2062
(SEQ ID NO:45)	Gdnfr	ATGAT.....	.....	.....GATTTT
(SEQ ID NO:54)	Hsgr-2	ATGAT.....	.....	.....GATTTT
(SEQ ID NO:55)	Hsgr-9	ATGATCATCA	TGATCATGAT	GATGATCATC
(SEQ ID NO:51)	29brc	ATGAT.....	.....	.....GATTTT



# FIG. 50

(SEQ ID NO:45)	Gdnfr	AACAGTTTTA	CTTCTGGCCT	TTCCTAGCTA	GAGAAGGAGT	TAAATATTCT	2113
(SEQ ID NO:54)	Hsgr-2	AACAGTTTTA	CTTCTGGCCT	TTCCTAGCTA	GAGAAGGAGT	TAAATATTCT	
(SEQ ID NO:55)	Hsgr-9	AACAGTTTTA	CTTCTGGCCT	TTCCTAGCTA	GAGAAGGAGT	TAAATATTCT	
(SEQ ID NO:51)	29brc	AACAGTTTTA	CTTCTGGCCT	TTCCTAGCTA	GAGAAGGAGT	TAAATATTCT	
(SEQ ID NO:45)	Gdnfr	AAGGTAACCTC	CCATATCTCC	TTTAATGACA	TTGATTCTTA	ATGATATAAA	2162
(SEQ ID NO:54)	Hsgr-2	AAGGTAACCTC	CCATATCTCC	TTTAATGACA	TTGATTCTTA	ATGATATAAA	
(SEQ ID NO:55)	Hsgr-9	AAGGTAACCTC	CCATATCTCC	TTTAATGACA	TTGATTCTTA	ATGATATAAA	
(SEQ ID NO:51)	29brc	AAGGTAACCTC	CCATATCTCC	TTTAATGACA	TTGATTCTTA	ATGATATAAA	
(SEQ ID NO:45)	Gdnfr	TTTCAGCCTA	CATTGATGCC	AAGCTTTTTT	GCCACAAAGA	AGATTCTTAC	2212
(SEQ ID NO:54)	Hsgr-2	TTTCAGCCTA	CATTGATGCC	AAGCTTTTTT	GCCACAAAGA	AGATTCTTAC	
(SEQ ID NO:55)	Hsgr-9	TTTCAGCCTA	CATTGATGCC	AAGCTTTTTT	GCCACAAAGA	AGATTCTTAC	
(SEQ ID NO:51)	29brc	TTTCAGCCTA	CATTGATGCC	AAGCTTTTTT	GCCACAAAGA	AGATTCTTAC	
(SEQ ID NO:45)	Gdnfr	CAAGAGTGGG	CTTTGTGGAA	ACAGCTGGTA	CTGATGTTCA	CCTTTATATA	2262
(SEQ ID NO:54)	Hsgr-2	CAAGAGTGGG	CTTTGTGGAA	ACAGCTGGTA	CTGATGTTCA	CCTTTATATA	
(SEQ ID NO:55)	Hsgr-9	CAAGAGTGGG	CTTTGTGGAA	ACAGCTGGTA	CTGATGTTCA	CCTTTATATA	
(SEQ ID NO:51)	29brc	CAAGAGTGGG	CTTTGTGGAA	ACAGCTGGTA	CTGATGTTCA	CCTTTATATA	



## FIG. 5P

(SEQ ID NO:45)	2263	Gdnfr	TGCTACTAGCA	TTTTCCACGC	TGATGTTTAT	GTACTGTAAA	CAGTTCTGCA	2312
(SEQ ID NO:54)		Hsgr-2	TGCTACTAGCA	TTTTCCACGC	TGATGTTTAT	GTACTGTAAA	CAGTTCTGCA	
(SEQ ID NO:55)		Hsgr-9	TGCTACTAGCA	TTTTCCACGC	TGATGTTTAT	GTACTGTAAA	CAGTTCTGCA	
(SEQ ID NO:51)		29brc	TGCTACTAGCA	TTTTCCACGC	TGATGTTTAT	GTACTGTAAA	CAGTTCTGCA	
(SEQ ID NO:45)	2313	Gdnfr	CTCTTGTACA	AAAGAAAAAA	CACCTGTCAC	ATCCAAATAT	AGTATCTGTC	2362
(SEQ ID NO:54)		Hsgr-2	CTCTTGTACA	AAAGAAAA				
(SEQ ID NO:55)		Hsgr-9	CTCTTGTACA	AAAGAAAA				
(SEQ ID NO:51)		29brc	CTCTTGTACA	AAAGAAAAAA	CACCTGTCAC	ATCCAAATAT	AGTATCTGTC	
(SEQ ID NO:45)	2363	Gdnfr	TTTTTCGTCAA	AATAGAGAGT	GGGGAATGAG	TGTGCCGATT	CAATACCTCA	2412
(SEQ ID NO:51)		29brc	TTTTTCGTCAA	AATAGAGAGT	GGGGAATGAG	TGTGCCGATT	CAATACCTCA	
(SEQ ID NO:45)	2413	Gdnfr	ATCCCTGAAC	GACACTCTCC	TAATCCTAAG	CCTTACCTGA	GTGAGAAGCC	2462
(SEQ ID NO:51)		29brc	ATCCCTGAAC	GACACTCTCC	TAATCCTAAG	CCTTACCTGA	GTGAGAAGCC	
(SEQ ID NO:45)	2463	Gdnfr	CTTTACCTAA	CAAAAGTCCA	ATATAGCTGA	AATGTCGCTC	TAATACTCTT	2512
(SEQ ID NO:51)		29brc	CTTTACCTAA	CAAAAGTCCA	ATATAGCTGA	AATGTCGCTC	TAATACTCTT	
(SEQ ID NO:45)	2513	Gdnfr	TACACATATG	AGGTTATATG	TAGAAAAAAA	TTTTTACTACT	AAATGATTTC	2562
(SEQ ID NO:51)		29brc	TACACATATG	AGGTTATATG	TAGAAAAAAA	TTTTTACTACT	AAATGATTTC	



## FIG. 5Q

(SEQ ID NO:45)	2563	Gdnfr	AACTATTGGC	TTTCTATATT	TTGAAAAGTAA	TGATATTGTC	TCATTTTTTT	2612
(SEQ ID NO:51)		29brc	AACTATTGGC	TTTCTATATT	TTGAAAAGTAA	TGATATTGTC	TCATTTTTTT	
(SEQ ID NO:45)	2613	Gdnfr	ACTGATGGTT	TAATACAAAA	TACACAGAGC	TTGTTTCCCC	TCATAAGTAG	2662
(SEQ ID NO:51)		29brc	ACTGATGGTT	TAATACAAAA	TACACAGAGC	TTGTTTCCCC	TCATAAGTAG	
(SEQ ID NO:45)	2663	Gdnfr	TGTTTCGCTCT	GATATGAACT	TCACAAATAC	AGCTCATCAA	AAGCAGACTC	2712
(SEQ ID NO:51)		29brc	TGTTTCGCTCT	GATATGAACT	TCACAAATAC	AGCTCATCAA	AAGCAGACTC	
(SEQ ID NO:45)	2713	Gdnfr	TGAGAAAGCCT	CGTGCTGTAG	CAGAAAGTTC	TGCATCATGT	GACTGTGGAC	2762
(SEQ ID NO:51)		29brc	TGAGAAAGCCT	CGTGCTGTAG	CAGAAAGTTC	TGCATCATGT	GACTGTGGAC	
(SEQ ID NO:45)	2763	Gdnfr	AGGCAGGAGG	AAACAGAAACA	GACAAGCATT	GTCCTTTTGTG	ATTGCTCGAA	2812
(SEQ ID NO:51)		29brc	AGGCAGGAGG	AAACAGAAACA	GACAAGCATT	GTCCTTTTGTG	ATTGCTCGAA	
(SEQ ID NO:45)	2813	Gdnfr	GTGCAAGCGT	GCATACCTGT	GGAGGGAAC	GGTGGCTGCT	TGTAAATGTT	2862
(SEQ ID NO:51)		29brc	GTGCAAGCGT	GCATACCTGT	GGAGGGAAC	GGTGGCTGCT	TGTAAATGTT	
(SEQ ID NO:45)	2863	Gdnfr	CTGCAGCATC	TCTTGACACA	CTTGTCATGA	CACAATCCAG	TACCTTGGTT	2912
(SEQ ID NO:51)		29brc	CTGCAGCATC	TCTTGACACA	CTTGTCATGA	CACAATCCAG	TACCTTGGTT	



FIG. 5R

		2913		2962
(SEQ ID NO:45)	Gdnfr	TTCAGGTTAT	CTGACAAAGG	CAGCTTTGAT
(SEQ ID NO:51)	29brc	TTCAGGTTAT	CTGACAAAGG	CAGCTTTGAT
				TGGGACATGG
				TGGGACATGG
				AGGCATGGGC
				AGGCATGGGC
		2963		
(SEQ ID NO:45)	Gdnfr	AGCCCGGAA		
(SEQ ID NO:51)	29brc	AGCCCGGAA		

FIG. 6

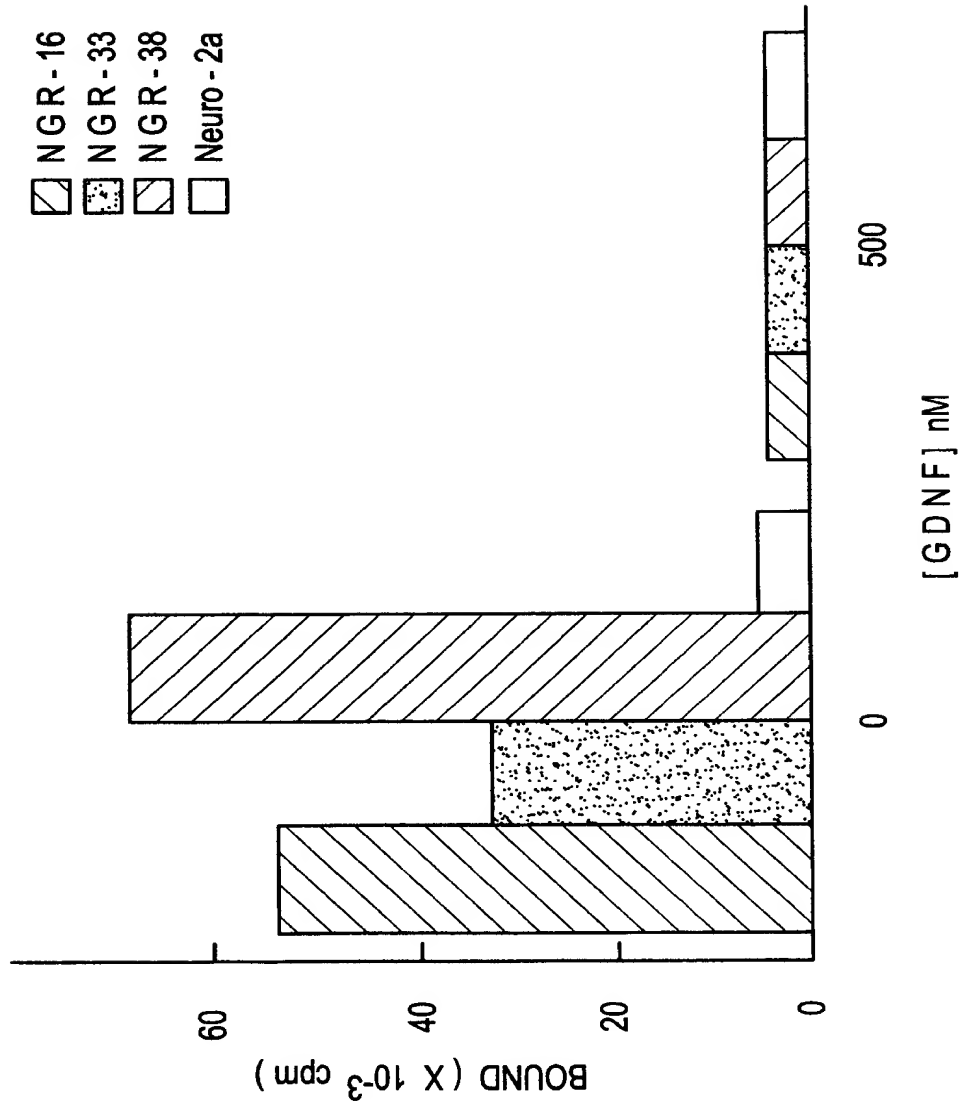






FIG. 7A

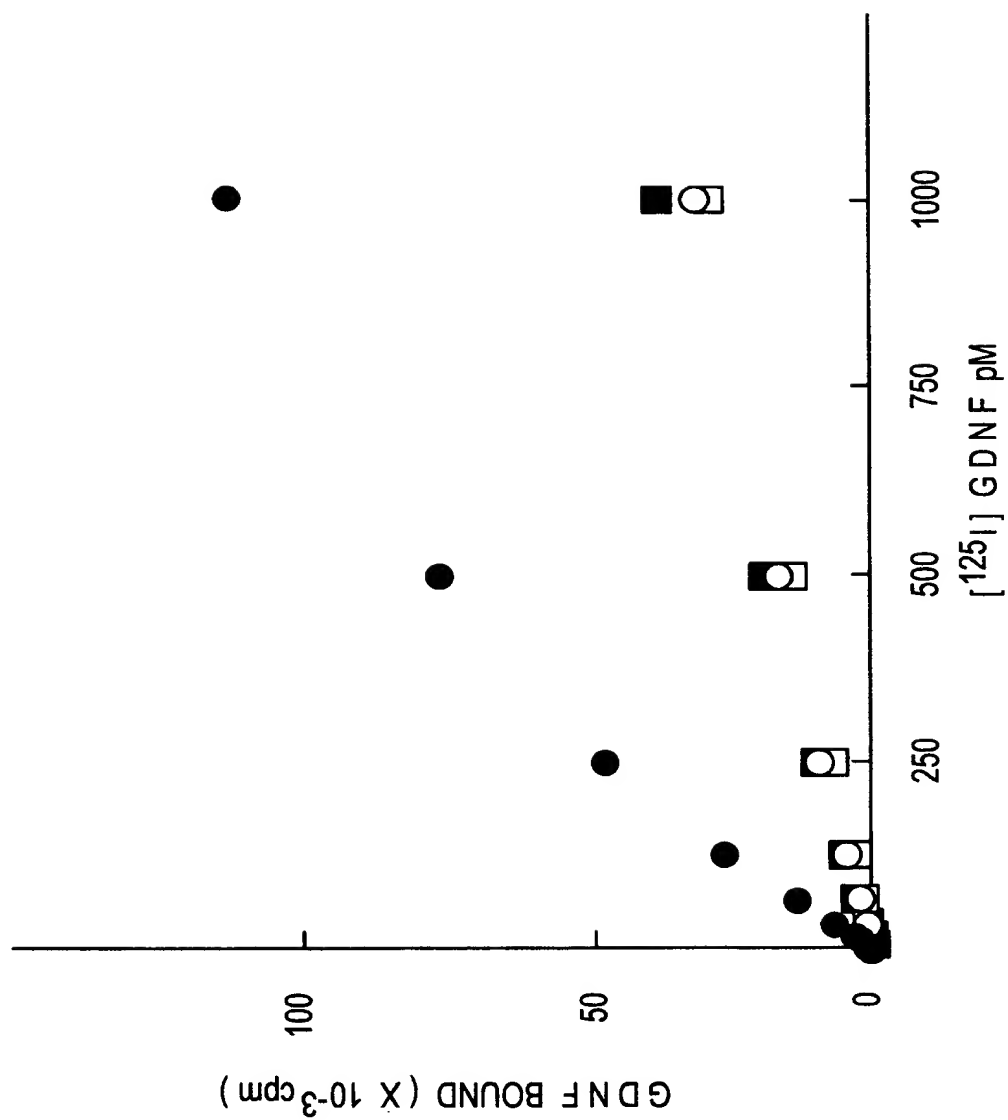




FIG. 7B

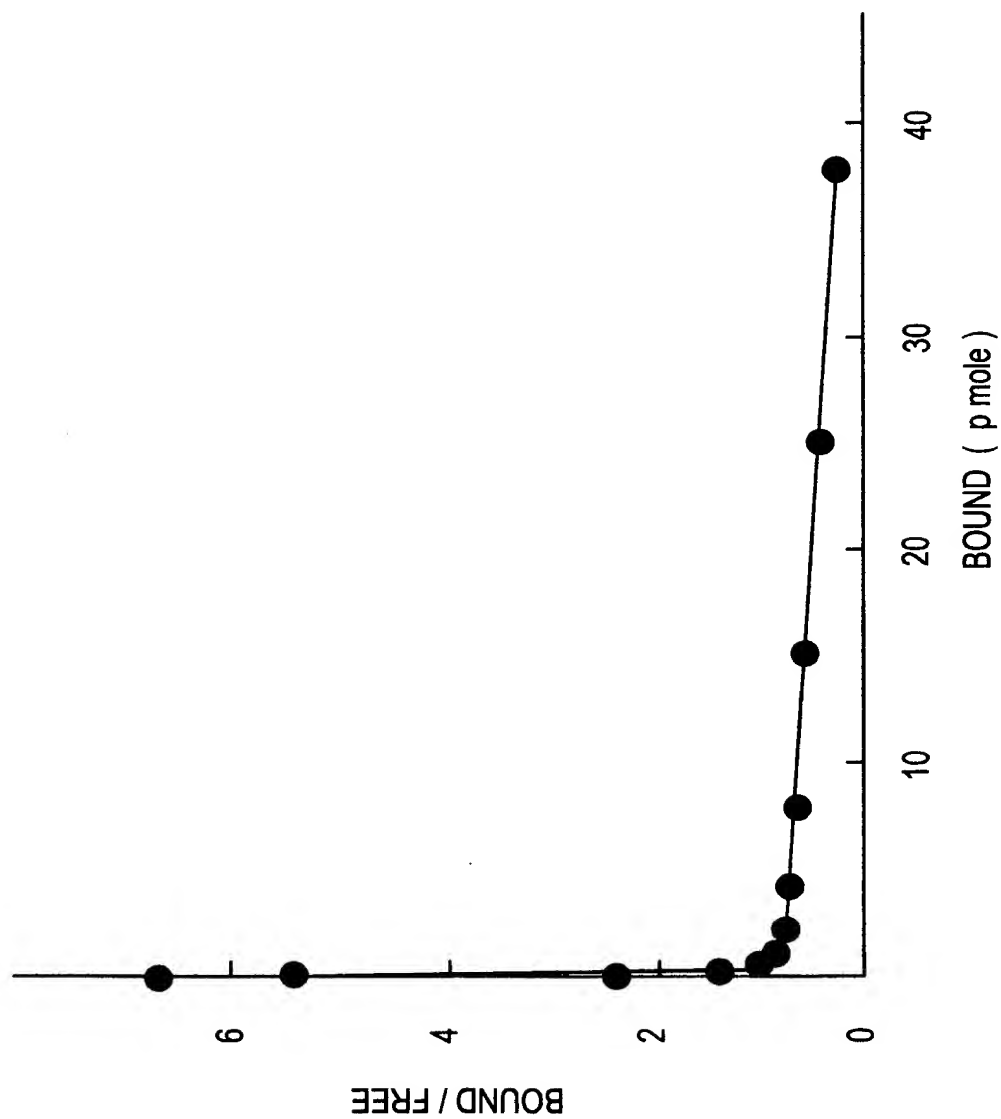


FIG.8

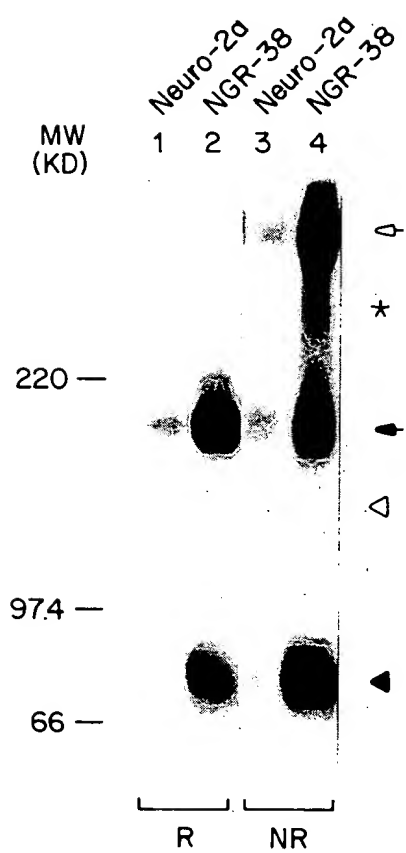
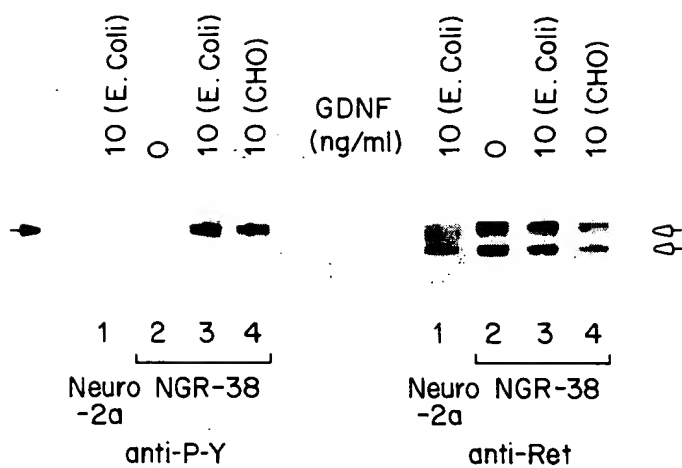
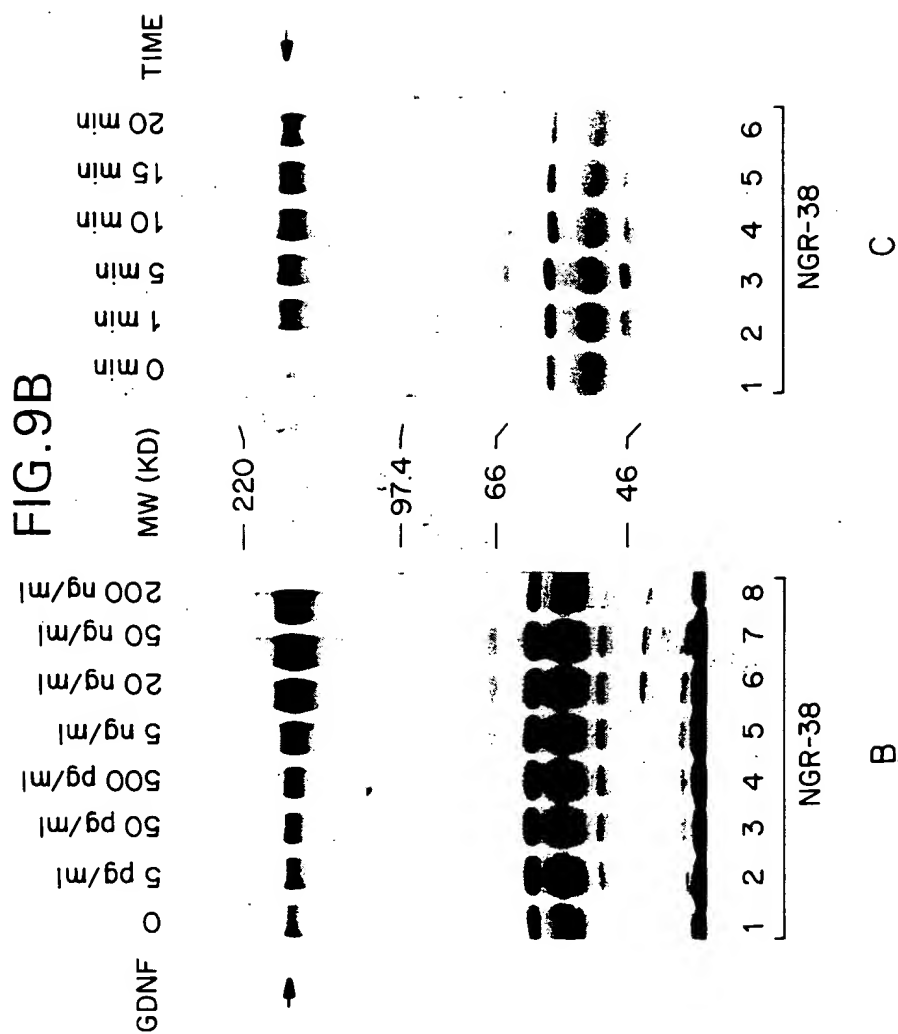


FIG.9A



A





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060904

FIG. 10

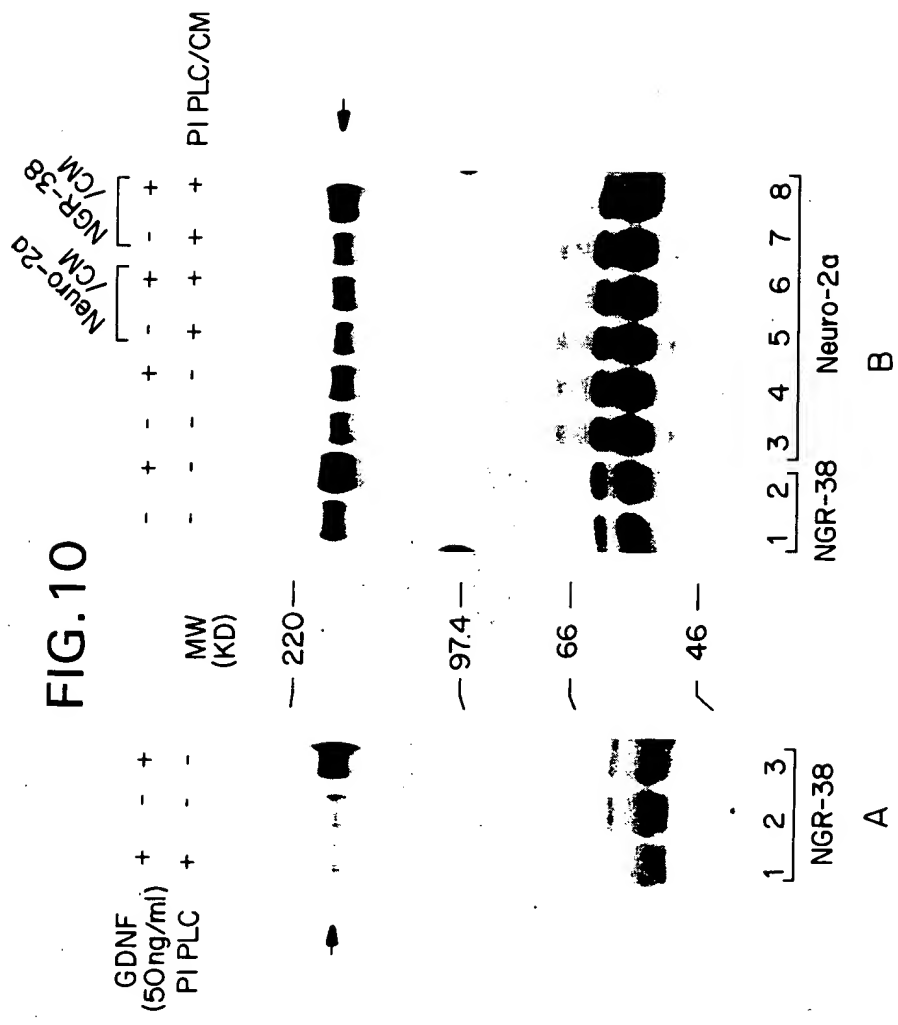


FIG. 11

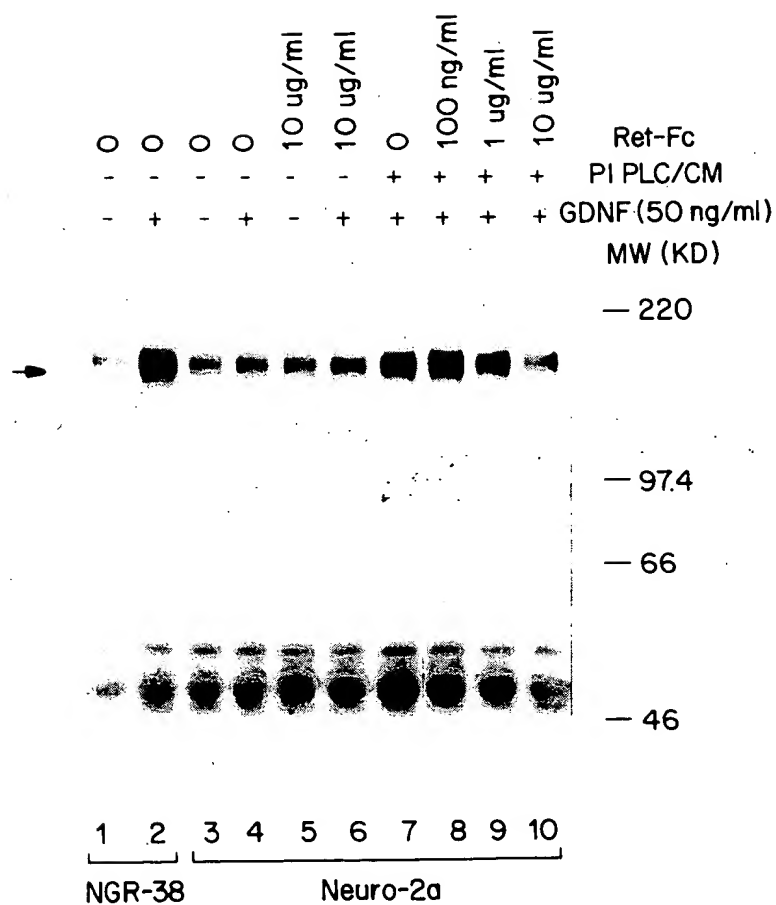


FIG.12

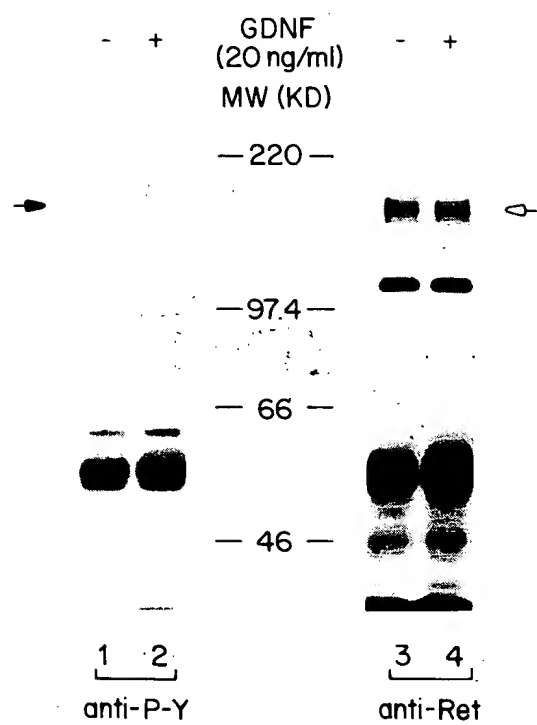
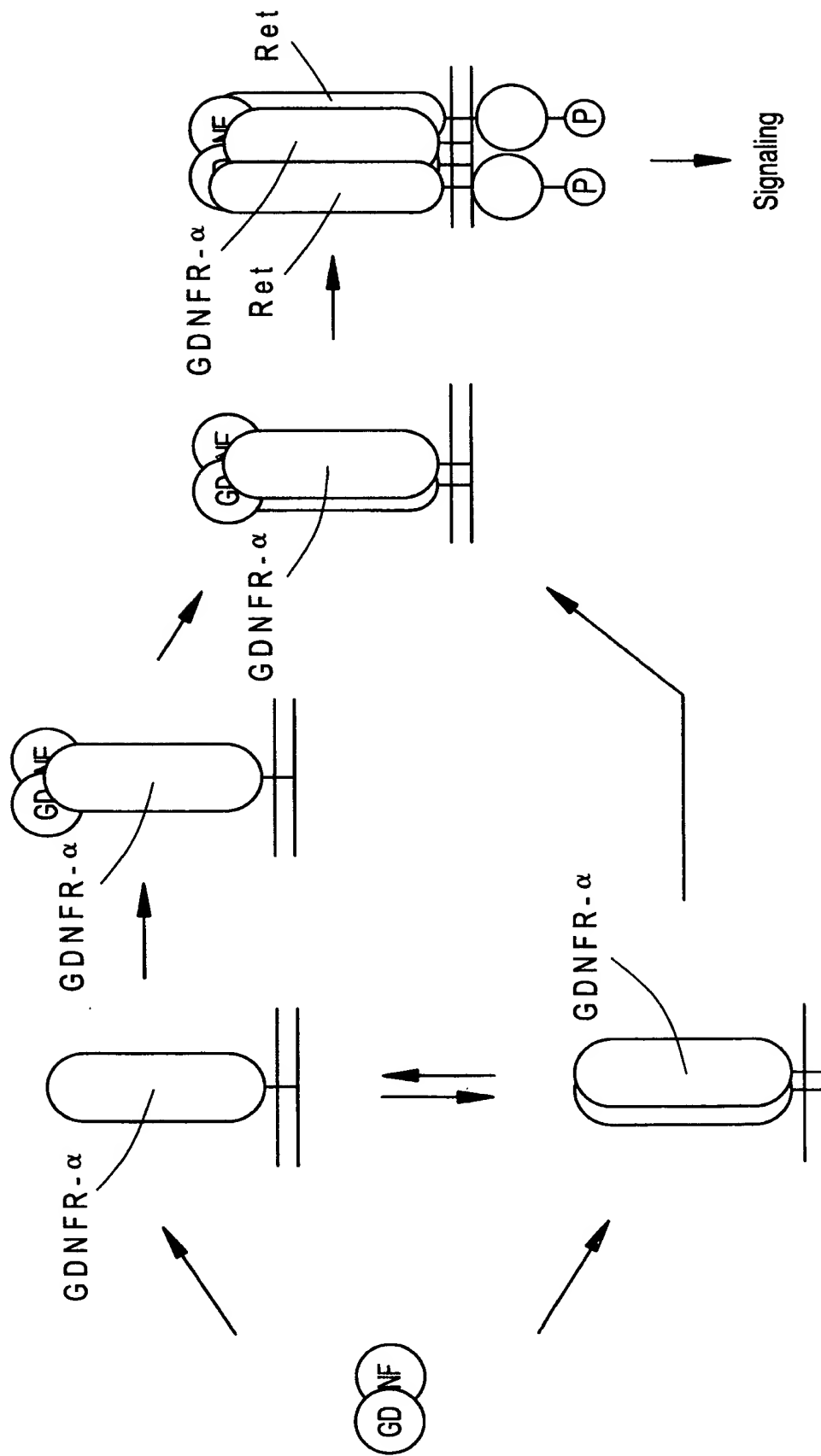




FIG. 13





## FIG.14A

Human GRR2

```
1  CATGAAGAAACCTCAGTAAGTCTCAGACTTGGCCCAAGGAGCCCACTAGTTACTCCCT 60
61  GGTCTGTTACAGAGGATCTGGCTATTACACTCAACAGCAAAAATTCAATTCAATCCCGCT 120
121 AAAGATATAAGAATCACTAGGAAKAATAAGCCAGAACTCAAGACAGAGAAATAGCATTAAGT 180
181 AGTTCCTTCAGTACAGTGAGCAGAAAGCTGGCCCACTCTACGACTCTAWAAGACTCAGAAAA 240
241 GCTTACTAGGACCWCTGGGCATWCCGGTGTCCTATGTGGGATTTTCGTAACGTCTTTGA 300
```



FIG.14C

721 TCTTCTATCTCCTCACTTCCCTATTACCCCTTTGAAGTGGGTACTGAATAGCCCGTTCCCA 780  
781 AGCAGAGGCCCTTTGTATACGGGGTGCTACAGTCGCCCTGGTGGAAACACCTTGGCAGAGT 840  
841 TGT TTGGTGCCAGGATGGGCCACTGAAGGCATCTGCTGTGGACACACACACACACA 900  
901 CACACACACACACACAGAGAGAGAGAGAGAAAGACACACGCACGAGAGACACAC 960  
961 GGTCAC TGGAA TTCCATTAGAAAAAGTGAGCCGAGCAAGGTTAGCGGAGAAAGATTTT 1020  
1021 TTTGAATCTTGTCCTTCGTCTTGGTGCGAAAGAGCGACTCCAGTCTCTCGTCCCTCGAAGC 1080  
1081 TCCGACTGGA TTGTTCTTGGGCGCTGACACCCGCTCTGTGGATTCTTTCTATTGCA TT 1140



FIG.14D

1141 TTATTCCGACCCCTCCCTCGCCGCTTCCTTCCAGCCCTTCACTCGCAAATCGCCTCTCT 1200  
1201 CCCCACCTCCCGAGGCCCTCCTGGGAAGCGCAGGGGAATTGGACCCCGGGGACTCAGG 1260  
1261 CCTTCCCGACGATTGGAGGGGAGGGCTGACCCCGAGGACTGGGCTGTGGCTTAGAAAGC 1320  
1321 CGATACACAGATACGCGTATATTGATTGTAGCGGGCAAGGGGGCGTCGAGAGGCAGCA 1380  
1381 GCCCATCGCCCGCCTCTCACCCCAACCCCTCCAGCCAGAGCGGAGAAATCGCAGGACTCGG 1440  
1441 GATCTTCATCGGGTGGACTAGCTGGGATCTCCGCATTGGATTGGGGCTGATTACCAC TG 1500



## FIG.14E

1501 CTTGGCTATTATTGTTGTTGTTACTACTATTATTTTATTTTACCCAAAGGGAGAAAGA . 1560

1561 CAAAAAACGGTGGGATTATTTAACAATGATCTTGGCAAAACGTCCTTCTGCCCCCTTCTTCT . 1620  
1 M I L A N V F C L F F F 12

1621 TTCTAGACGACACCCCTCCGCTCTTTGGCCAGCCCTTCCCTCCCTGCAGGGCCCCGAGCTCC . 1680  
13 L D D T L R S L A S P S S L Q G P E L H 32

1681 ACGGCTGGCGCCCCAGTGGACTGTGTCCGGGCCAATGAGCTGTGTGCCCGCGAATCCA . 1740  
33 G W R P P V D C V R A N E L C A A E S N 52

1741 ACTGCAGCTCTCGCTACCGCACTCTGCGGCAGTGCCTGGCAGGCCGCGACCGCAACACCA . 1800  
53 C S S R Y R T L R Q C L A G R D R N T M 72



FIG.14F

1801	TGCTGGCCAACAAGAGTGCCAGCGCGCTTGAGGTCTTGCAAGAGAGAGCCCGCTGTACG	1860
73	L A N K E C Q A A L E V L Q E S P L Y D	92
1861	ACTGCCGCTGCAAGCGGGGCATGAAGAAGAGCTGCAGTGTCTGCAGATCTACTGGAGCA	1920
93	C R C K R G M K K E L Q C L Q I Y W S I	112
1921	TCCACCTGGGGCTGACCGAGGGTGAGGAGTTCTACGAAGCCTCCCCCTATGAGCCGGTGA	1980
113	H L G L T E G E F Y E A S P Y E P V T	132
1981	CCTCCCGCCTCTCGGACATCTTCAGGCTTGCTTCAATCTTCTCAGGGACAGGGCAGACC	2040
133	S R L S D I F R L A S I F S G T G A D P	152
2041	CGGTGGTCAGCGCCAAGAGCAACCATTCCTGTGATGCTGCCAAGCCTGCAACCTGAATG	2100
153	V V S A K S N H C L D A A K A C N L N D	172
2101	ACAACTGCAAGAAGCTGGCTCCTCCTACATCTCCATCTGCAACCGGAGATCTCGCCCA	2160
173	N C K K L R S S Y I S I C N R E I S P T	192

FIG.14G

2161 CCGAGCGCTGCAACCGCCGCAAGTGCCACAAGGCCCTGCGCCAGTTCTTCGACCGGTGC 2220  
193 E R C N R R K C H K A L R Q F F D R V P 212

2221 CCAGCGAGTACACCTACCGCATGCTCTTCTGCTCCTGCTGCAAGACCAGGCGTGCGCTGAGC 2280  
213 S E Y T Y R M L F C S C Q D Q A C A E R 232

2281 GCCGCCGGCAACCATCCTGCCCGAGCTGCTCCTATGAGGACAAGGAGAACCCAACTGCC 2340  
233 R R Q T I L P S C S Y E D K E K P N C L 252

2341 TGGACCTGCGTGCGGTGCGCGGACTGACCACCTGTGTGTCGGTCCCGGCTGGCCGACTTCC 2400  
253 D L R G V C R T D H L C R S R L A D F H 272

2401 ATGCCAATTGTCGAGCCTCCTACCAGACGGTCAACAGCTGCCCTGCGGACAATTACCAGG 2460  
273 A N C R A S Y Q T V T S C P A D N Y Q A 292





## FIG.14H

2461	CGTGTCTGGGCTCTTATGCTGGCATGATTGGGTTTGACATGACACCTAACTATGTGGACT	2520
293	C L G S Y A G M I G F D M T P N Y V D S	312
2521	CCAGCCCCACTGGCATCGTGGTGTCCTCCCTGGTGCGAGCTGTCTGCGCAGCGCGGAACATGG	2580
313	S P T G I V V S P W C S C R G S G N M E	332
2581	AGGAGGAGTGTGAGAAAGTTCCCTCAGGGACTTCACCGAGAACCCCATGCCCTCCGGAACGCCA	2640
333	E E C E K F L R D F T E N P C L R N A I	352
2641	TCCAGGCCCTTTGGCAACGGCACGAACGTGAACGTGTCCCCCAAAGGCCCTCGTTCCAGG	2700
353	Q A F G N G T N V N V S P K G P S F Q A	372
2701	CCACCCAGGCCCTCGGGTGGAAGACGCCCTTCTTTGCCAGATGACCTCAGTGACAGTA	2760
373	T Q A P R V E K T P S L P D D L S D S T	392



FIG.14I

2761	CCAGCTTGGGACCAGTGTTCATCACCACCTGCACGTCTGTCCAGGAGCAGGGGCTGAAGG	2820
393	S L G T S V I T T C T S V Q E Q G L K A	412
2821	CCAACAACCTCCAAGAGTTAAGCATGTGTCTTCACAGAGCTCACGACAAATATCATCCAG	2880
413	N N S K E L S M C F T E L T T N I I P G	432
2881	GGAGTAACAAGGTGATCAAAACCTAACTCAGGCCCCAGCAGCCAGACCGTCGGCTGCCT	2940
433	S N K V I K P N S G P S R A R P S A A L	452
2941	TGACCGTGTCTGTCTGTGATGTGAAACTGGCCTTGTAGGCTGTGGGAACCGAGTCAG	3000
453	T V L S V L M L K L A L *	464
3001	AAGATTTTGTGAAGCTACGCAGACAAGAACAGCCGCTGACGAAATGGAACACACACAG	3060
	. . . . .	



FIG.14J

3061 ACACACACACCTTGCAAAAAAATTGTTTTTCCACCTTGTCGCTGAACCTGTCTC 3120  
3121 CTCCCAGGTTTCTCTCTGGAGAGTTTGTAAACCAACAGACAAGCAGGCAGGCAGC 3180  
3181 CTGAGAGCTGGCCCAGGGGTCCCCCTGGCAGGGGAACTCTGGTGCCGGGAGGGCAGCAG 3240  
3241 GCTCTAGAAATGCCCTTCACTTTCTCCTGGTGTTTTTCTCTCTGGAACCTTCTGAAGCAG 3300  
3301 AGACCGGACAAGAGCCTGCAGCGGAAGGACTCTGGGCTGTGCTGAGGCTGGCTGGGG 3360  
3361 CAGGACAACACAGCTGCTTCCCCAGGCTGCCCACTCTGGGACCCGCTGGGGCTGGCAG 3420  
3421 AGGGCATCGGTACGGGGCAGCGGGGCTGGCCATGAGGGTCCACCTCAGCCCTTTGGC 3480



FIG.14K

3481 TTCAAGGATGGAGATGGTTTGGCCCTCCCTCTCTGTGCCCTCGGGTGGGCTGGTGGGTCTG . . . 3540

3541 CAGCTGGTGTGGGAACTTCCCCACGGATGGCGGTGGAGGGGTTCCGCACCGTGCTGGGCT . . . 3600

3601 CCCCCTGACTGTAGCACGGAGTGTGGGGCTGGGGGCCAGCTCCAGGAGGGCTTGAGAGC . . . 3660

3661 TCAGCCCTGCCCTGGGAGAGCCCTTGTGGCGAGGCATTAAACTTGGGCACCAGCTTCTTTC . . . 3720

3721 TCGGTGGCAGAAATTTGAAGTCAGAGAGAAACGGTCCCTTTGTGGCTTCTTTGCTTTCT . . . 3780

3781 CGTGGGTCCCTTTGGCAGGCCCTCCCTTTGGGGAGAGGGGAGAGACCACAGCCGGGTG . . . 3840

3841 TGTGTCTGCAGCACCGTGGGCCCTCAAGCTTCCCTGCTGTCTTCTCCCTCCCTCCCTTT . . . 3900



FIG.14L

3901 CCCCTTCTCTTTCCTCATTTCCCTAGACGTACGTCAACTGTATGTACATACCGGGCTCC 3960  
3961 TCTCCTAACATATATGTATATACACATCCATATACATATATATTGTGTGTTTCCCCCTTCT 4020  
4021 TTCCCTTTTTTAAGCAACAACAACTATGGAAATAATACCCCAACAGATGAGCGAAATGTA 4080  
4081 TTATTGTAAAGTTTATTTTTTTTAAATACTGTTGTCTATAATGGGGAATAAGGACATTGGC 4140  
4141 CCCGCAGTGCCCTGCCCCAGTCAGCCCTGGCTGGGCTCTGGTGGGGGCTCCTGATCCGCAT 4200  
4201 CCAAGCTTAACCAAGGCTCCAATAAACGTGCG 4232



# FIG.15A

Human GRR3

1	CAAGTCAAAGGTTTAATCATGATCCAAGAGCCCCAGAGAGACTTTAGGACAATAATAGGAA	60
61	TAAAGCAAGGCCACAGGCTCCAGCTCCTGATGCCCCAGATGTTCCGGCAGGATCCGGGGAC	120
121	AGGGCAGTGCAGGCAGTAGTTTCCATCCTCCATCCAGGGAGGAGCGGAGCGCGG	180
181	AGCCCGGCGCCTACAGCTCGCCCATGGTGCGCCCCCTGAACCCCGGACCGCTGCCCGCCCGT	240
1	M V R P L N P R P L P P V	13
241	AGTCCTGATGTTGCTGCTGCGCGCGCTCGCCGCTGCCTCTCGCAGCCGGAGACCC	300
14	V L M L L L L P P S P L P L A A G D P	33



FIG.15B

301 CCTTCCACAGAAAGCCGACTCATGAACAGCTGTCTCCAGGCCAGGAGGAAGTGCCAGGC 360  
34 L P T E S R L M N S C L Q A R R K C Q A 53  
361 TGATCCACCTGCAGTGTGCCCTACCAACCTGGATTCCCTGCACCTCTAGCATAAGCAC 420  
54 D P T C S A A Y H H L D S C T S S I S T 73  
421 CCCACTGCCCTCAGAGGAGCCTTCGGTCCCTGCTGACTGCCCTGGAGGCACACAGCAACT 480  
74 P L P S E E P S V P A D C L E A A Q Q L 93  
481 CAGGAACAGCTCTCTGATAGGCTGCATGTGCCACCGCGCATGAAGAACCCAGGTGCGCTG 540  
94 R N S S L I G C M C H R R M K N Q V A C 113  
541 CTTGGACATCTATTGGACCGTTACCCGTGCCCGCAGCCCTTGGTAACTATGAGCTGGATGT 600  
114 L D I Y W T V H R A R S L G N Y E L D V 133



FIG.15C

601	CTCCCCCTATGAAGACACAGTGACCAGCAACCCCTGGAAAATGAATCTCAGCAAACTGAA	660
134	S P Y E D T V T S K P W K M N L S K L N	153
661	CATGCTCAAACCACTCAGACCTCTGCCCTCAAGTTTGCCATGCTGTGTACTCTCAATGA	720
154	M L K P D S D L C L K F A M L C T L N D	173
721	CAAGTGACCGGCTGCGCAAGGCTACGGGAGGCGTGCTCCGGGCCCCACTGCCAGCG	780
174	K C D R L R K A Y G E A C S G P H C Q R	193
781	CCACGTCTGCCTCAGGCAGCTGCTCACTTCTTCGAGAAGCGCGCGAGCCCCACGCGCA	840
194	H V C L R Q L L T F F E K A A E P H A Q	213
841	GGGCTGCTACTGTGCCCATGTGCCCCCAACGACCGGGGCTGCGGGAGCGCGCGCAA	900
214	G L L L C P C A P N D R G C G E R R N	233





## FIG.15D

901	CACCATCGCCCCCAACTGCGCGCTGCCGCTGTGGCCCCCAACTGCCCTGGAGCTGCGGCG	960
234	T I A P N C A L P P V A P N C L E L R R	253
961	CCCTCTGCTTCTCCGACCCGCTTTCAGATCAGCGCTGGTGATTTCCAGACCCACTGCCA	1020
254	L C F S D P L C R S R L V D F Q T H C H	273
1021	TCCCATGGACATCCTAGGAACCTGTGCAACAGAGCAGTCCAGATGTCTACGAGCATACCT	1080
274	P M D I L G T C A T E Q S R C L R A Y L	293
1081	GGGGCTGATTGGGACTGCCATGACCCCAACTTTGCCAGCAATGTCAACACCAAGTGTGC	1140
294	G L I G T A M T P N F A S N V N T S V A	313
1141	CTTAAGCTGCACCTGCCGAGGCAGTGGCAACCTGCAGGAGGAGTGTGAAATGCTGGAAGG	1200
314	L S C T C R G S G N L Q E E C E M L E G	333



FIG.15E

1201	GTTCCTCTCCACAACCCCTGCCTCACGGAGGCCATTGCAGCTAAGATGCGTTTTCACAG	1260
334	F F S H N P C L T E A I A A K M R F H S	353
1261	CCAACTCTCTCCAGGACTGGCCACACCCCTACCTTTGCTGTGATGGCACACCAGAATGA	1320
354	Q L F S Q D W P H P T F A V M A H Q N E	373
1321	AAACCCTGCTGTGAGGCCACAGCCCTGGGTGCCCTCTCTTTCTCCTGCACGCTTCCCTT	1380
374	N P A V R P Q P W V P S L F S C T L P L	393
1381	GATTCTGCTCCTGAGCCCTATGGTAGCTGGACTTCCCCAGGGCCCTCTTCCCCCTCCACCAC	1440
394	I L L S L W *	400
1441	ACCCAGGTGGACTTGCAGCCCAAGGGGTGAGGAAGGACAGCAGCAGGAAGGAGGTGC	1500



# FIG.15F

1501 AGTGCGCAGATGAGGGCACAGGAGAAGCTAAGGGTTATGACCTCCAGATCCTTACTGGTC 1560  
1561 CAGTCCTCATTCCTCCACCCCATCTCCACTTCTGATTCATGCTGCCCTCCTTGGTGGC 1620  
1621 CACAATTTAGCCATGTCATCTGGTGGTGACCAGCTCCACCAAGCCCCCTTTGTGAGCCCTT 1680  
1681 CCTCTTGACTACCAGGATCACCCAGAAATCTAATAAGTTAGCCCTTTCTCTATTGCAATCCAG 1740  
1741 ATTAGGGTTAGGGTAGGGAGGACTGGGTGTTCTGAGGCAGCCTAGAAAGTCATTCTCCTT 1800  
1801 TGTGAAGAAGGCTCCTGCCCCCTCGTCTCCTCCTCTGAGTGGAGGATGGAATACTACTGC 1860  
1861 CTGCACTGCCCTGTCCCCGGATCCTGCCGAACATCTGGGCATCAGGAGCTGGAGCCCTGTG 1920



## FIG.15G

1921 GGCCTTGCTTTATTCCTATTATTGTCCTAAAGTCTCTCTGGGCTCTTGGATCATGATTAA . . . 1980

1981 ACCTTTGACTG . 1991



# FIG.16A

Rat GRR2

1	CGGGCCGCTCGACCTTGACCATGCAGACACTTTTTCAGGCCCTCTGCTGGTGTGAAGTT	60
61	GGCAGATACAAGCAAGGCCCGAAAGGGTCTCAGCTTCTCTCCTGGCCCTCCTGGACT	120
121	GAGTAGGCTTGCTTCTGGTTGTCTTCTAAAGGCACGGTGATACAGAAATGATGAGACTAG	180
181	GCTGGAGGGGCTTTCTGCTTCTGCTGTGTGACCTTGAGTTATCTCCCTTCGTTGGATC	240
241	CGAGCTTTCCTGGAAATATGATGTTGAATATGAATATGAGTTCTGCCCTAAGGTCCAGACAG	300



FIG.16B

301 GCTCTGAGGGTTAACTGACTTTTGGAGCCCTTCAAATCAATACCTTGGATGGAGTGGGGGT 360

361 TTGTCCAATGGGAGTTGAGGCAAGATCCCTTTGCATAAGCCCTTGCCACATCATGTTGAAG 420

421 CCAATGCCAATTCTGTCTGGACTATTGGCACTCTTACCTTTCCAGCAGTTTTCAGTGAAGGCCT 480

481 TCCTGGATTATCATTTCTGTGTTCCACTGCCCTAGGATTGTGCTCAAGAGGAAATGAATGT 540

541 GAACCATGGTTAGGGAGTATGGCCAACCAAGTTGGGTCTGTGTGACCTTGGTCTTG 600  
1 M V V G E Y G Q P G W V C V D L G L G 19

601 GTGTTCTTTTGTAAAGTGGGTGAGAAGTTCCTTCAAACCTTAGGCCTACATTGGGGTC 660  
20 V L L C K V G E K F L Q T L G L H W G Q 39

FIG.16C

661 AGAGACTGTGGTGGCCCTCATTCATGCTTGTCTTCCCTTCCCTACTACCCAGACGAAACCC 720  
40 R L W W P S F M L V F P S H Y P D E T L 59

721 TCCGCTCTTGGCCAGCCCTTCCCTGCAGGGCTCTGAGCTCCACGGCTGGCGCCCCC 780  
60 R S L A S P S S L Q G S E L H G W R P Q 79

781 AAGTGACTGTGTCCGGGCCAATGAGCTGTGTGCGGCTGAATCCAATGCAGCTCCAGGT 840  
80 V D C V R A N E L C A A E S N C S S R Y 99

841 ACCGCACCCCTTCGGCAGTGCCTGGCAGGCCGGGATCGCAATACCATGCTGGCCAATAAGG 900  
100 R T L R Q C L A G R D R N T M L A N K E 119

901 AGTGCCAGGCAGCCCTGGAGGTCTTGCAGGAAGCCCACTGTATGACTGCCGCTGCAAGC 960  
120 C Q A A L E V L Q E S P L Y D C R C K R 139

. . . . .



## FIG.16D

961	GGGGCATGAAGAAGGAGCTGCAGTGTCTGCAGATCTACTGGAGCATCCATCTGGGGCTGA	1020
140	G M K K E L Q C L Q I Y W S I H L G L T	159
1021	CAGAGGTGAGGAGTTCTATGAAGCTTCCCCCTATGAGCCTGTGACCTCGCGCCTCTCGG	1080
160	E G E E F Y E A S P Y E P V T S R L S D	179
1081	ACATCTCAGGCTCGCTTCAATCTTCTCAGGGACAGGGACAGACCCGGCGTCAGTACCA	1140
180	I F R L A S I F S G T G T D P A V S T K	199
1141	AAAGCAACCACTGCCTGGATGCCGCCAAGCCTGCAACCTGAATGACAACCTGCAAGAAGC	1200
200	S N H C L D A A K A C N L N D N C K K L	219
1201	TTCGCTCCTCTTATATCTCCATCTGCAACCGTGAGATCTCTCCACCGAACGCTGCAACC	1260
220	R S S Y I S I C N R E I S P T E R C N R	239





FIG.16E

1261	GCCGCAAGTGCCACAAGGCTCTGCGCCAGTCTTTGACCGTGTGCCGAGCGAGTATACCT	1320
240	R K C H K A L R Q F F D R V P S E Y T Y	259
1321	ACCGCATGCTCTTCTGCTCCTGTCAGGACCAGGCATGTGCTGAGCGTCGCCGCAACCA	1380
260	R M L F C S C Q D Q A C A E R R Q T I	279
1381	TCCTGCCCAGTTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCCCTGGACCTGCCGAGCC	1440
280	L P S C S Y E D K E K P N C L D L R S L	299
1441	TGTGTCGTACAGACCACCTGTGCCCGGTCCCGACTGGCAGATTCCACGCCCAACTGTCGAG	1500
300	C R T D H L C R S R L A D F H A N C R A	319
1501	CCTCCTACCGGACAATCACCAGCTGTCTGCGGACAACCTACCAGGCATGCTGGGCTCCT	1560
320	S Y R T I T S C P A D N Y Q A C L G S Y	339



FIG.16F

1561	ATGCTGGCATGATTGGGTTTGATATGACACCCAACTATGTGGACTCCAACCCACGGGCA	1620
340	A G M I G F D M T P N Y V D S N P T G I	359
1621	TCGTGGTGTCCTCCCTGGTGCAATTGTCGTGGCAGTGGGAACATGGAAGAAGAGTGTGAGA	1680
360	V V S P W C N C R G S G N M E E C E K	379
1681	AGTTCCTCAGGGACTTCACGGAAACCCATGCCCTCCGGAATGCCATTTCAGGCCTTTGGTA	1740
380	F L R D F T E N P C L R N A I Q A F G N	399
1741	ATGGCACAGATGTGAACATGTCTCCCAAAGGCCCTCACTCCAGCTACCCAGGCCCTC	1800
400	G T D V N M S P K G P S L P A T Q A P R	419
1801	GGGTGGAGAAGACTCCTTCACTGCCAGATGACCTCAGTGACAGCACCAAGCCTGGGGACCA	1860
420	V E K T P S L P D D L S D S T S L G T S	439
1861	GTGTCATCACCACCTGCACATCTATCCAGGAGCAAGGGCTGAAGGCCAACAACTCCAAAG	1920



## FIG.16G

440 V I T T C T S I Q E Q G L K A N N S K E 459

1921 AGTTAAGCATGTGCTTCACAGAGCTCACGACAAACATCAGTCCAGGGAGTAAAGGTGA 1980  
460 L S M C F T E L T T N I S P G S K K V I 479

1981 TCAAACTTAACAGGCTCCAGCAGAGCCAGACTGTGCGCTGCCCTTGACTGCCCTCCAC 2040  
480 K L N S G S S R A R L S A A L T A L P L 499

2041 TCCTGATGCTGACCTTGGCCCTTGTAGGCCCTTTGGAACCCAGCACAAAGTTCTTCAAGCA 2100  
500 L M L T L A L \* 506

2101 ACCCAGATATGAAC TCCCGCTGACAAATGGAAACACACGCATACACACATGCCACACA 2160

2161 CAGACACACACAGACACACACACACACATACAGACGTCGACGGCGGC 2215





FIG.17B

241 CAGCACCTGGACTCCTGCACCCCCAGTCTCAGCAGTCCACTGCCCTCAGGGAGTCTGCC 300  
59 Q H L D S C T P S L S S P L P S G E S A 78

301 ACATCTGCAGCGTGCCTTGAAGCAGCACAGCAACTCAGGAACAGCTCTCTCATAGACTGC 360  
79 T S A A C L E A A Q Q L R N S S L I D C 98

361 AGTGCCACCGCGCATGAAGCACCAAGCTACCTGTCTGGACATTATTGGACCGTTCAC 420  
99 R C H R R M K H Q A T C L D I Y W T V H 118

421 CCTGTCCGAAGCCTTGGTGACTACGAGTTGGACGTCTCACCCCTATGAAGACACAGTGACC 480  
119 P V R S L G D Y E L D V S P Y E D T V T 138

481 AGCAAAACCCTGGAAATGAATCTCAGCAAGCTGAGCATGCTCAAAACCAGACTCCGACCTC 540  
139 S K P W K M N L S K L S M L K P D S D L 158

FIG.17C

541 TGCCTCAAATTGCTATGCTGTGTACTCTTAACGACAAGTCCGACCGCCTCCGAAAGGCC 600  
159 C L K F A M L C T L N D K C D R L R K A 178

601 TACGGGAGGCGTGCTCAGGGATCCGCTGCCAGCGCCACCTCTGCTAGCTCAGCTGCGC 660  
179 Y G E A C S G I R C Q R H L C L A Q L R 198

661 TCCTTCTTCGAGAAGCGGCAGAGTCCACGCTCAGGGCCTGCTGTGTCCTGTGCA 720  
199 S F F E K A A E S H A Q G L L C P C A 218

721 CCCGAAGATGCGGGCTGTGGGAGCGCGCGCAACACCATCGCCCCAGTTGGCCCTC 780  
219 P E D A G C G E R R R N T I A P S C A L 238

781 CCGTCTGTGGCCCCAACTGCCCTAGATCTTCGGAGCTTCTGCCGTGCGGACCCCTGTGC 840  
239 P S V A P N C L D L R S F C R A D P L C 258

. . . . .

# FIG.17D

841	AGATCAGCCTGATGGACTTCCAGACCCACTGCCACCCCTATGGACATCCTCGGACTTGT	900
259	R S R L M D F Q T H C H P M D I L G T C	278
901	GCAACTGAGCAGTCCAGATGCTCGGGGCATACCTGGGGCTAATTGGGACTGCCATGACC	960
279	A T E Q S R C L R A Y L G L I G T A M T	298
961	CCAAACTTCATCAGCAAGGTCAACACTACTGTTGCCTTAGGCTGTACCTGCCGAGGCAGT	1020
299	P N F I S K V N T T V A L G C T C R G S	318
1021	GGCAACCTGCAGGACGAGTGTGAACAGCTGGAAGTCCTTCTCCAGAACCCCTGCCTC	1080
319	G N L Q D E C E Q L E K S F S Q N P C L	338
1081	ATGGAGGCCATTGCGGCTAAATGCGTTTCCACAGACAACACTCTTCTCCAGGACTGGCGG	1140
339	M E A I A A K M R F H R Q L F S Q D W A	358



## FIG.17E

1141 GACTCTACTTTTCTGTGATGCAGCAGCAGAACAGCAGCCCTGCTCTGAGGCCCCAGCTC 1200  
359 D S T F S V M Q Q Q Q N S S P A L R P Q L 378

1201 AGGCTACCCGTTCTGTCTTTCTTTCATCCCTTACCTTGATTCTGCTGCAGACCCCTCTGGTAA 1260  
379 R L P V L S F F I L T L I L L Q T L W \* 397

1261 CTGGGCTCCCCTCAGGGTCCTTTGTCCCTCTCCACCACACCCAGACCGACTTGCAGCCTGTG 1320

1321 ATGGGAGAGAAATGCTGGCCTCTGGAAGAGATGCAACCAGGCTCACTGCACATCCTGT 1380

1381 CTGCTCCAGATGAGGTCTTGGAAGAGCGAGGGCTGTGACCCGTTCAGAAATCCTGAGCGGC 1440

1441 CAGCTTTCAAACCTCTCCTACTTACTCCTGCTTGGGCTGCTCCTCCCTAGGACCTTGTA 1500





## FIG.17F

1501 TCCAGTTGGCTGTATATTGTGGTGGTATTAGCTTCCCACCTCCAGCCCTTCTTCCCTGT 1560

1561 TTCCCAGGACCAACCAGGGCTAATGACTCACTCATTCCTGGTTGCCCTTCTCCAGGAAGGC 1620

1621 AGGCTGAGGGTTCTGAGGCAGCTGAGAAAGATGGTCCCTTTGTGAGGAAGGCTGGTGGTC 1680

1681 CAACCGTCGACGGGGCCGC 1699

## FIG.18A

Alignment of the Amino Acid Sequences of GDNFRs

1			50
Mgdnfr	~~~~~	~~~~MFLATL YFVLPLLDLL MSAEVSG.GD RLDCVKASDQ	
Rgdnfr	~~~~~	~~~~MFLATL YFALPLLDLL MSAEVSG.GD RLDCVKASDQ	
Hgdnfr	~~~~~	~~~~MFLATL YFALPLLDLL LSAEVSG.GD RLDCVKASDQ	
Hgrr2	~~~~MILANV	FCLFFFLLDDT LRSLASPSSL QGPELHGWRP PVDCVRANEL	
Rgrr2	~~~~~ML	VFPSHYPDET LRSLASPSSL QGSELHGWRP QVDCVRANEL	
Hgrr3	MVRPLNPRPL	PPVLMLLLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK	
Rgrr3	MGLSRSPRPP	PLVILLVLS L...WLPLGT GNSLPTENRL VNSCTQARRK	



## FIG.18B

	51	100
Mgdnfr	CLKEQSCSTK YRTLQCVAG KETNFSLTSG LEAKDECRSA MEALKQKSLY	
Rgdnfr	CLKEQSCSTK YRTLQCVAG KETNFSLTSG LEAKDECRSA MEALKQKSLY	
Hgdnfr	CLKEQSCSTK YRTLQCVAG KETNFSLTSG LEAKDECRSA MEALKQKSLY	
Hgrr2	CAAESNCSSR YRTLQCLAG RDRNTML... ..ANKECQAA LEVLQESPLY	
Rgrr2	CAAESNCSSR YRTLQCLAG RDRNTML... ..ANKECQAA LEVLQESPLY	
Hgrr3	CQADPTCSAA YHLDSTSS ISTPLP.SEE PSVPADCLEA AQQLRNSSLI	
Rgrr3	CEANPACKAA YHLDSTPS LSSPLP.SGE SATSAACLEA AQQLRNSSLI	



FIG.18C

	101		150
Mgdnfr	NCRCKRGMKK EKNCLRIYWS MYQSL.QGND LLEDSPYEPV NSRLSDIFRA		
Rgdnfr	NCRCKRGMKK EKNCLRIYWS MYQSL.QGND LLEDSPYEPV NSRLSDIFRA		
Hgdnfr	NCRCKRGMKK EKNCLRIYWS MYQSL.QGND LLEDSPYEPV NSRLSDIFRV		
Hgrr2	DCRCKRGMKK ELQCLQIYWS IHLGLTEGEE FYEASPYEPV TSRLSDIFRL		
Rgrr2	DCRCKRGMKK ELQCLQIYWS IHLGLTEGEE FYEASPYEPV TSRLSDIFRL		
Hgrr3	GCMCHRRMKN QVACLDIYWT VHRARSLGNY ELDVSPYE..		.....DTVTS
Rgrr3	DCRCHRRMKH QATCLDIYWT VHPVRSGLDY ELDVSPYE..		.....DTVTS



FIG.18D

151		200
Mgdnfr	VPFISDVFQQ VEHISKGNNC LDAAKACNLD DTCKKYRSAY ITPCTTSMs.	
Rgdnfr	VPFISDVFQQ VEHISKGNNC LDAAKACNLD DTCKKYRSAY ITPCTTSMs.	
Hgdnfr	VPFISDVFQQ VEHIPKGNNC LDAAKACNLD DICKKYRSAY ITPCTTSVS.	
Hgrr2	ASIFSGTGAD PVVSAKSNHC LDAAKACNLD DNCKKLRSSY ISICNREISP	
Rgrr2	ASIFSGTGTD PAVSTKSNHC LDAAKACNLD DNCKKLRSSY ISICNREISP	
Hgrr3	KPWKMNL SKL NMLKPDSDLC LKFAMLC TLN DKCDRLRKAY GEACS.....	



FIG.18E

Rgrr3 KPWKMNLSKL SMLKPDS DLC LKFAMLCTLN DKCDRLRKAY GEACS.....

201 250

Mgdnfr NEVCNRRKCH KALRQFFDKV PAKHSYGMLF CSC..RDVAC TERRRQTIVP

Rgdnfr NEVCNRRKCH KALRQFFDKV PAKHSYGMLF CSC..RDIAC TERRRQTIVP

Hgdnfr NDVCNRRKCH KALRQFFDKV PAKHSYGMLF CSC..RDIAC TERRRQTIVP

Hgrr2 TERCNRRKCH KALRQFFDRV PSEYTYRMLF CSC..QDQAC AERRRQTILP

Rgrr2 TERCNRRKCH KALRQFFDRV PSEYTYRMLF CSC..QDQAC AERRRQTILP

Hgrr3 GPHCQRHVCL RQLLTFFEKA AEPHAQGLLL CPCAPNDRGC GERRRNTIAP

Rgrr3 GIRCQRHLCL AQLRSFFEKA AESHAQGLLL CPCAPEDAGC GERRRNTIAP



## FIG.18F

	251		300
Mgdnfr	VCSYEERERP	NCLNLQDSCK	TNYICRSRLA DFFTNCQPES RSVSNCLKEN
Rgdnfr	VCSYEERERP	NCLSLQDSCK	TNYICRSRLA DFFTNCQPES RSVSNCLKEN
Hgdnfr	VCSYEEREKP	NCLNLQDSCK	TNYICRSRLA DFFTNCQPES RSVSSCLKEN
Hgrr2	SCSYEDKEKP	NCLDLRGVCR	TDHLCRSRLA DFHANCRAZY QTVTSCPADN
Rgrr2	SCSYEDKEKP	NCLDLRSLCR	TDHLCRSRLA DFHANCRAZY RTITSCPADN
Hgrr3	NCALPP.VAP	NCLELRRLCF	SDPLCRSRLV DFQTHCHP.. MDILGTCATE
Rgrr3	SCALPS.VAP	NCLDLRSFCR	ADPLCRSRLM DFQTHCHP.. MDILGTCATE



## FIG.18G

301

350

Mgdnfr	YADCLLAYSG	LIGTVMTPNY	VDSS..SLSV	APWCDCSNSG	NDLEDCLKFL
Rgdnfr	YADCLLAYSG	LIGTVMTPNY	VDSS..SLSV	APWCDCSNSG	NDLEDCLKFL
Hgdnfr	YADCLLAYSG	LIGTVMTPNY	IDSS..SLSV	APWCDCSNSG	NDLEECCLKFL
Hgrr2	YQACLSYAG	MIGFDMTPNY	VDSSPTGIVV	SPWCSCRGSG	NMEEECEKFL
Rgrr2	YQACLSYAG	MIGFDMTPNY	VDSNPTGIVV	SPWCNCRGSG	NMEEECEKFL
Hgrr3	QSRCLRAYLG	LIGTAMTPNF	ASNVTTSVAL	S..CTCRGSG	NLQEECEMLE
Rgrr3	QSRCLRAYLG	LIGTAMTPNF	ISKVNTTVAL	G..CTCRGSG	NLQDECEQLE





FIG.18H

	351		400
Mgdnfr	NFFKDNTCLK NAIQAFNGS DVTMWQPAP. PVQTTTATTT TAFRIKNKPS		
Rgdnfr	NFFKDNTCLK NAIQAFNGS DVTMWQPAP. PVQTTTATTT TAFRVKNKPL		
Hgdnfr	NFFKDNTCLK NAIQAFNGS DVTVWQPAF. PVQTTTATTT TALRVKNKPL		
Hgrr2	RDFTENPCLR NAIQAFNGT NVNVSPKGP. SFQATQAPRV EKTPSLPDDL		
Rgrr2	RDFTENPCLR NAIQAFNGT DVNMSPKGP. SLPATQAPRV EKTPSLPDDL		
Hgrr3	GFFSHNPCLT EAIAAKMRFH SQLFSQDWPH PTFAVMAHQN ENPAVRPQPW		
Rgrr3	KSFSQNPCLM EAIAAKMRFH RQLFSQDWAD STFSVMQQQN SSPALRPQLR		



## FIG.18I

401		450
Mgdnfr	GPACSENEIP THVLPPCANL QAQKLKSNVS GSTHLCCLSDN DYGKDGLAGA	
Rgdnfr	GPAGSENEIP THVLPPCANL QAQKLKSNVS GSTHLCCLSDS DFGKDGLAGA	
Hgdnfr	GPAGSENEIP THVLPPCANL QAQKLKSNVS GNTHLCISNG NYEKEGL.GA	
Hgrr2	SDSTS...LG TSVITTTCTSV QEQGLKANNS KELSMCFTTEL TTNIIPGSNK	
Rgrr2	SDSTS...LG TSVITTTCTSI QEQGLKANNS KELSMCFTTEL TTNISPGSKK	
Hgrr3	VPSLFSCCTLP LILLLSLW~~ ~~~~~~	
Rgrr3	LPVLSFFILT LILLQTLW*~ ~~~~~~	



FIG.18J

	451		490
Mgdnfr	SSHITTKSMA APPSCGLSSL PVMVFTALAA	LLSVSLAETS	
Rgdnfr	SSHITTKSMA APPSCSLSSL PVLMLTALAA	LLSVSLAETS	
Hgdnfr	SSHITTKSMA APPSCGLSPL LVLVVTALST	LLSLTETS~~	
Hgrr2	VIKPNGPSR ARPSAALTVL SVLMLKLAL*	~~~~~	
Rgrr2	VIKLSGSSR ARLSAALTAL PLLMLTLAL*	~~~~~	
Hgrr3	~~~~~	~~~~~	
Rgrr3	~~~~~	~~~~~	

# FIG.19A

## GDNFR Family of Receptors

1	50
Consensus	MV..l...p .pp...m.l. llslalPl... .lqgael.g. .Rl..dCv.A.
Hgdnfr	MFLAT LYFALPLLLDL LLsAEVSGGD RL..DCVKAS
Rgdnfr	MFLAT LYFALPLLLDL LMSAEVSGGD RL..DCVKAS
Hgrr2	MILANVF CLFFFLDDTL RSLASPSS.. LQPELHW. RPPVDCVRAN
Rgrr2	MLV FPSHYPDETL RSLASPSS.. LQSELHW. RPQVDCVRAN
Hgrr3	MVRPLNPRPL PPVLMLLLL LPPS.PLP.L AAGDPLPTES RLMNSCLQAR
Rgrr3	MGLSRSPR PPPLVILLV LSLWLPLG.. .TGNSLPTEN RLVNSCTQAR



# FIG.19B

	51		100
Consensus	..C.ae..Cs ..YrtLrqC. ag...nt.La sg.E..... C..A.e.L..		
Hgdnfr	DQCLKEQSCS TKYRTLrQCV AGKETNFSLA SGLEAKDE.. CRSAMEALKQ		
Rgdnfr	DQCLKEQSCS TKYRTLrQCV AGKETNFSLT SGLEAKDE.. CRSAMEALKQ		
Hgrr2	ELCAAESNCS SRYRTLrQCL AGRDRNTMLA NK.E..... CQAALEVLQE		
Rgrr2	ELCAAESNCS SRYRTLrQCL AGRDRNTMLA NK.E..... CQAALEVLQE		
Hgrr3	RKCQADPTCS AAYHHLDST ..SSISTPLP SE.EPSVPAD CLEAAQQLRN		
Rgrr3	KKCEANPACK AAYQHLDST ..PSLSSPLP SG.ESATSAA CLEAAQQLRN		



## FIG.19C

Consensus	ssLydCrCkR	gMKke...CL.	IYws.h...l.	.Gn...le.SP	YEp.VtSrls	150
Hgdnfr	KSLYNCRCKR	GMKKEKNCLR	IYWSMYQSLQ	.GNDLLEDSP	YEP.VNSRLS	
Rgdnfr	KSLYNCRCKR	GMKKEKNCLR	IYWSMYQSLQ	.GNDLLEDSP	YEP.VNSRLS	
Hgrr2	SPLYDCRCCKR	GMKKELQCLQ	IYWSIHLGLT	EGEEFYEASP	YEP.VTSRLS	
Rgrr2	SPLYDCRCCKR	GMKKELQCLQ	IYWSIHLGLT	EGEEFYEASP	YEP.VTSRLS	
Hgrr3	SSLIGCMCHR	RMKNQVACLD	IYWTVHRARS	LGNYELDVSP	YEDTVTSKPW	
Rgrr3	SSLIDCRCHR	RMKHQATCLD	IYWTVHPVRS	LGDYELDVSP	YEDTVTSKPW	

# FIG.19D

151

200

Consensus	difr...s..s	....d.....	ksn.CLdaAk	aCnLnD.Ckk	lRsaYi..C.
Hgdnfr	DIFRVVPFIS	DVFQQVEHIP	KGNNCLDAAK	ACNLDDICKK	YRSAYITPCT
Rgdnfr	DIFRAVPFIS	DVFQQVEHIS	KGNNCLDAAK	ACNLDDTCKK	YRSAYITPCT
Hgrr2	DIFRLASIFS	GTGADPVVSA	KSNHCLDAAK	ACNLNDNCKK	LRSSYISICN
Rgrr2	DIFRLASIFS	GTGTDPAVST	KSNHCLDAAK	ACNLNDNCKK	LRSSYISICN
Hgrr3	KMNL..SKLN	MLKPD.....	.SDLCLKFAM	LCTLNDKCDR	LRKAYGEAC.
Rgrr3	KMNL..SKLS	MLKPD.....	.SDLCLKFAM	LCTLNDKCDR	LRKAYGEAC.



## FIG.19E

Consensus	...	S..erCn	RrkChkaLrq	FFdkvp..h.	ygmLfCsC..	.D.aC.ERRR	250
Hgdnfr	TSVS.	NDVCN	RRKCHKALRQ	FFDKVPAKHS	YGMLFCSC..	RDIACTERRR	
Rgdnfr	TSMS.	NEVCN	RRKCHKALRQ	FFDKVPAKHS	YGMLFCSC...	RDIACTERRR	
Hgrr2	REISPTERCN	RRKCHKALRQ	FFDRVPSEYT	YRMLFCSC..	QDQACAERRR		
Rgrr2	REISPTERCN	RRKCHKALRQ	FFDRVPSEYT	YRMLFCSC..	QDQACAERRR		
Hgrr3	...	SG.PHCQ	RHVCLRQLLT	FFEKAAEPHA	QGLLLCPCAP	NDRGCCERRR	
Rgrr3	...	SG.IRCQ	RHLCLAQLRS	FFEKAAESHA	QGLLLCPCAP	EDAGCGERRR	





## FIG.19F

Consensus	qTI.PsCsye ..ekPNCLdL r..CrtD.lC RSRLaDF.tn C....r.v.s	251	300
Hgdnfr	QTIVPVCSYE EREKPNCLNL QDSCKTNYIC RSRLADFFTN CQESRSVSS		
Rgdnfr	QTIVPVCSYE EREKPNCLSL QDSCKTNYIC RSRLADFFTN CQESRSVSN		
Hgrr2	QTILPSCSYE DKEKPNCLDL RGVCRDHL C RSRLADFHAN CRASYQTVTS		
Rgrr2	QTILPSCSYE DKEKPNCLDL RSLCRTDHL C RSRLADFHAN CRASYRTITS		
Hgrr3	NTIAPNC.AL PPVAPNCLEL RRLCFSDPLC RSRLVDFQTH C.HPMDILGT		
Rgrr3	NTIAPSC.AL PSVAPNCLEL RSFCRADPLC RSRLMDFQTH C.HPMDILGT		



## FIG.19G

301

350

Consensus	C.a.ny..CL	.ay.Gligt.	MTPNyvdss.	t...VapwC.	CrgSGN...ee
Hgdnfr	CLKENYADCL	LAYSGLIGTV	MTPNYIDSSS	..LSVAPWCD	CSNSGNDLEE
Rgdnfr	CLKENYADCL	LAYSGLIGTV	MTPNYVDSSS	..LSVAPWCD	CSNSGNDLED
Hgrr2	CPADNYQACL	GSYAGMIGFD	MTPNYVDSSP	TGIVVSPWCS	CRGSGNMEEE
Rgrr2	CPADNYQACL	GSYAGMIGFD	MTPNYVDSNP	TGIVVSPWCN	CRGSGNMEEE
Hgrr3	C.ATEQSRCL	RAYLGLIGTA	MTPNFASNVN	TS..VALSCT	CRGSGNLQEE
Rgrr3	C.ATEQSRCL	RAYLGLIGTA	MTPNFISKVN	TT..VALGCT	CRGSGNLQDE



FIG.19H

	351		400
Consensus	Cekfl.ff..	NpCL.nAIqA fgng.....p.fsv .....t.t.a	
Hgdnfr	CLKFLNFFKD	NTCLKNAIQA FGNGS....D VTVWQPAPPV QTTATTTA	
Rgdnfr	CLKFLNFFKD	NTCLKNAIQA FGNGS....D VTMWQPAPPV QTTATTTA	
Hgrr2	CEKFLRDFTE	NPCLRNAIQA FGNGTNV... ..NVSP KGPSFQATQA	
Rgrr2	CEKFLRDFTE	NPCLRNAIQA FGNGTDV... ..NMSP KGPSLPATQA	
Hgrr3	CEMLEGFFSH	NPCLTEAIAA KMRFHSQLFS QDWPHTFAV MAHQENPAV	
Rgrr3	CEQLEKSFSQ	NPCLMEAIAA KMRFHRQLFS QDWADSTFSV MQQONSSPAL	



## FIG.19I

401	Consensus	.rv...PsL. ....s....l. t.v...C..l Q.Q.LK.N.S .e....Cf.e.l	450
	Hgdnfr	LRVKNKP.LG PAGSENEIP. THVLPPCANL QAQKLKSNVS GNTHLCISNG	
	Rgdnfr	FRVKNKP.LG PAGSENEIP. THVLPPCANL QAQKLKSNVS GSTHLCCLSDS	
	Hgrr2	PRVEKTPSLP DDLSDSTSLG TSVITTTCTSV QEQLKANNS KELSMCFTTEL	
	Rgrr2	PRVEKTPSLP DDLSDSTSLG TSVITTTCTSI QEQLKANNS KELSMCFTTEL	
	Hgrr3	RPQPWVPSLF SCTLPLILL SLW	
	Rgrr3	RPQLRLPVLS FFILTILLQ TLW	
451	Consensus	ttn.....sg. ...i....s... A.ps.aL..L pvlmltála. LLS.....S	499
	Hgdnfr	NYEKEGL.GA SSHITTKSMA APPSCGLSPL LVRVVTALST LLSLTETS	
	Rgdnfr	DFGKDGLAGA SSHITTKSMA APPCSLSSL PVLMLTALAA LLSVSLA	
	Hgrr2	TTNIIPGSNK VIKPNSGPSR ARPSAALTVL SVLMLK.LAL	
	Rgrr2	TTNISPGSKK VIKLNSGSSR ARLSAALTAL PLLMLTLAL	

FIG. 20A

Human GDNFR $\alpha$   
Rat GDNFR $\alpha$   
Human GRR2  
Rat GRR2

MFLATLYFALPLLDLLLSAEVSGGDRLLDCVKASDQCLKE  
MFLATLYFALPLLDLLMSAEVSGGDRLLDCVKASDQCLKE  
MILANVECLFEFFLDDTLRSLASPSLQGPFLHGWRRPVD CVRANEI CAAE  
MLVFP SHYPDET LRS LASPSLQGS ELHGWRRPQVD CVRANEI CAAE

Human GDNFR $\alpha$   
Rat GDNFR $\alpha$   
Human GRR2  
Rat GRR2

QSCSTKYRTL RQCVAGKETNFSLASGLEAKDECRSAMEALKQKSLYNCR  
QSCSTKYRTL RQCVAGKETNFSLTSGLEAKDECRSAMEALKQKSLYNCR  
SNCSRYRTL RQCLAGRDRN.....TMLANKECQAALEV LQESP LYDCRC  
SNCSRYRTL RQCLAGRDRN.....TMLANKECQAALEV LQESP LYDCRC

Human GDNFR $\alpha$   
Rat GDNFR $\alpha$   
Human GRR2  
Rat GRR2

KRGMKKEKNCLRIYWSMYQSL.QGNDLLEDSPYEPVNSRLSDIFRVVPFI  
KRGMKKEKNCLRIYWSMYQSL.QGNDLLEDSPYEPVNSRLSDIFRVVPFI  
KRGMKKHLQCLQIYWSIHGLGLTEGEEFYFASPYEPVTSRLSDIFRLASIF  
KRGMKKELQCLQIYWSIHGLGLTEGEEFYFASPYEPVTSRLSDIFRLASIF

FIG. 20B

Human GDNFR $\alpha$

Rat GDNFR $\alpha$

Human GRR2

Rat GRR2

SDVFEQQVEHI PKGNNCLDAAKACNLDDICKKYRSAYITPCTTSVS.NDVVC  
SDVFEQQVEHI SKGNNCLDAAKACNLDDICKKYRSAYITPCTTSMS.NEVVC  
SGTGADPVS AKSNHCLDAAKACNLNDNCKKLRSYISICNREISPTERC  
SGTGTDDAVSTKSNHCLDAAKACNLNDNCKKLRSYISICNREISPTERC

Human GDNFR $\alpha$

Rat GDNFR $\alpha$

Human GRR2

Rat GRR2

NRRKCHKALRQFFDKVP AKHSYGM LFCSCRDIACTERRRQTIVPVCSYEE  
NRRKCHKALRQFFDKVP AKHSYGM LFCSCRDIACTERRRQTIVPVCSYEE  
NRRKCHKALRQFFDRVPSEYTYRMLFCSCQDQACAEERRRQTILPSCSYED  
NRRKCHKALRQFFDRVPSEYTYRMLFCSCQDQACAEERRRQTILPSCSYED

Human GDNFR $\alpha$

Rat GDNFR $\alpha$

Human GRR2

Rat GRR2

REKPNCLNLQDSCKTNYICRSRLADFFTNCPESRSVSSCLKENYADCIL  
REKPNCLNLQDSCKTNYICRSRLADFFTNCPESRSVSNCLKENYADCIL  
KEKPNCLDLRGVCRTHLCRSRLADFFHANCRA SYQTIVTSCPADNYQACILG  
KEKPNCLDLRSLCRTDHL CRSRLADFFHANCRA SYRITITSCPADNYQACILG

Human GDNFR $\alpha$

Rat GDNFR $\alpha$

Human GRR2

Rat GRR2

AMSGLIGTVMTPNYIDSS..SLSVAPWDCSN SGNDLEECLKFLEFFKDN  
AMSGLIGTVMTPNYVDSS...SLSVAPWDCSN SGNDLEEDCLKFLEFFKDN  
SYAGMIGFDMTPNYVDSSPTGIVVSPWCS CRGSGNMEEEECEKFLRDFTEN  
SYAGMIGFDMTPNYVDSSNPTGIVVSPWCSN CRGSGNMEEEECEKFLRDFTEN



**FIG. 20C**

Human GDNFR $\alpha$   
Rat GDNFR $\alpha$   
Human GRR2  
Rat GRR2

TCLKNAIQAFNGSDV	IVWQPAF	PVQTTTATTTT	ATTTTALRVKNKPLCPAGSEN
TCLKNAIQAFNGSDV	IVWQPAF	PVQTTTATTTT	ATTTTALRVKNKPLCPAGSEN
PCLRNAIQAFNGTINV	NSPKGPSFQA	ICAPRVEKTPSLPDDLSDSTS	..
PCLRNAIQAFNGTINV	NSPKGPSLPATC	APRVEKTPSLPDDLSDSTS	..

Human GDNFR $\alpha$   
Rat GDNFR $\alpha$   
Human GRR2  
Rat GRR2

EIPTHVLPPCANIQAQKLKSNVSGNTHLCISNGNVEKEGL.GASSHITTK  
EIPTHVLPPCANIQAQKLKSNVSGNTHLCISDSDFGKDCIACASSHITTK  
.LGTSVITTCOTSVQEQGLKANNSKELSMCFTELTNNIIPGSNKVIKENSG  
.LGTSVITTCOTSIQEOGLKANNSKELSMCFTELTNNISPGSKKVIKLNSSG

Human GDNFR $\alpha$   
Rat GDNFR $\alpha$   
Human GRR2  
Rat GRR2

SMAAPPSCGISPLLVVVT.ALSTLL..SILTETS  
SMAAPPSCSLSLPLVLMIT.ALALLSVSIAETS  
PSRARPSAALTVLSVLMKIAL  
SSRARLSAALTALPLLMITIAL



FIG. 21A

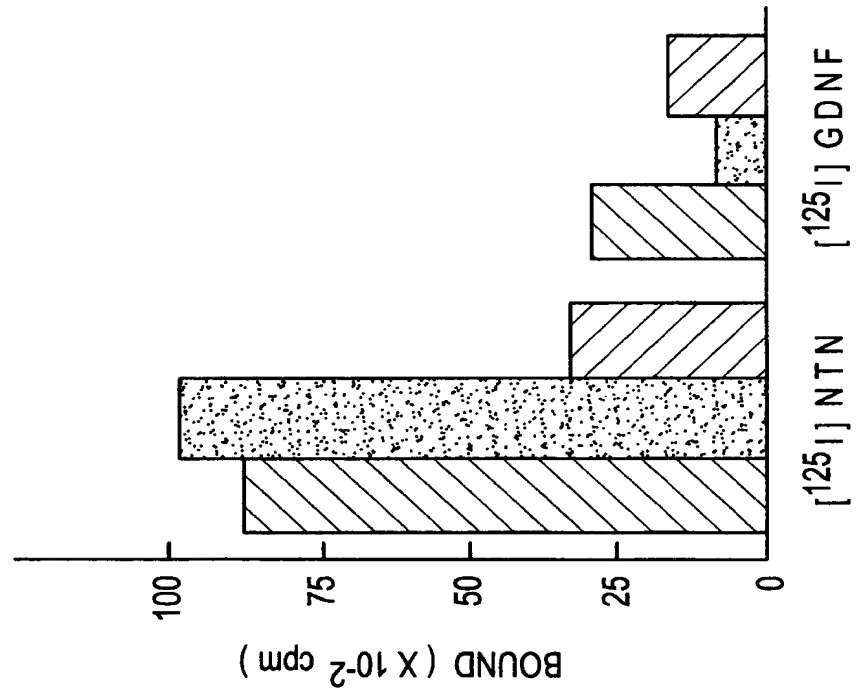


FIG. 21B

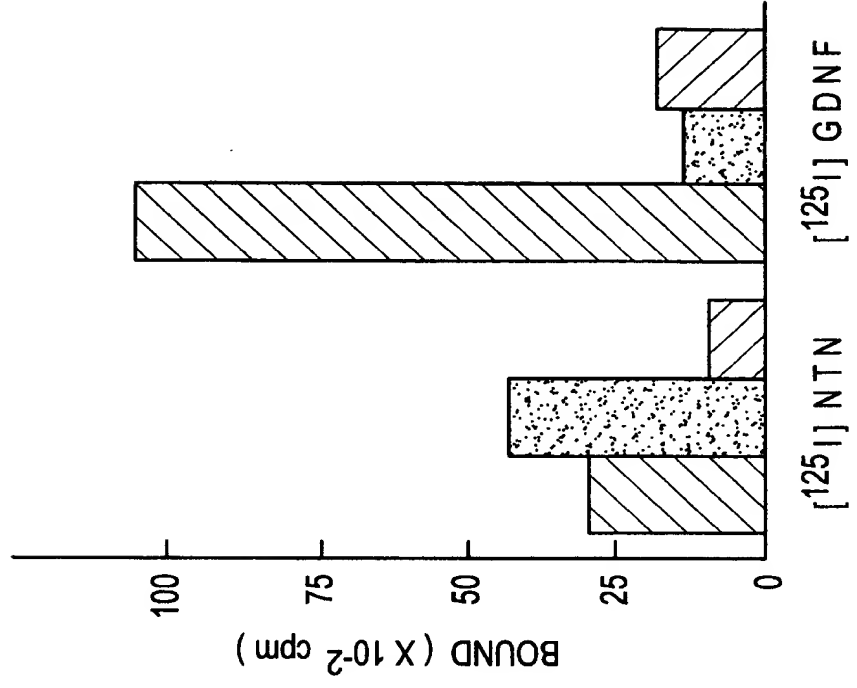




FIG.22

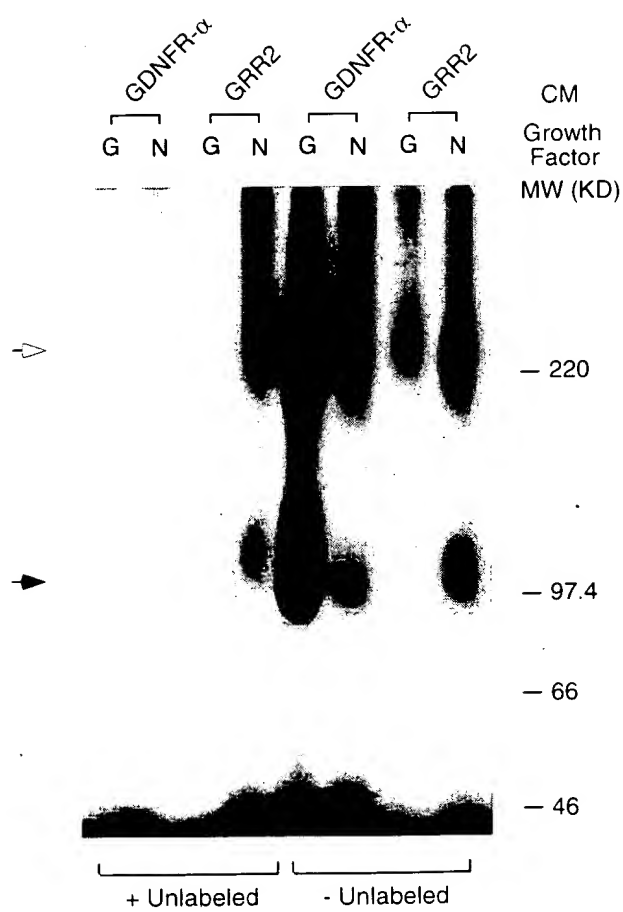


FIG.23

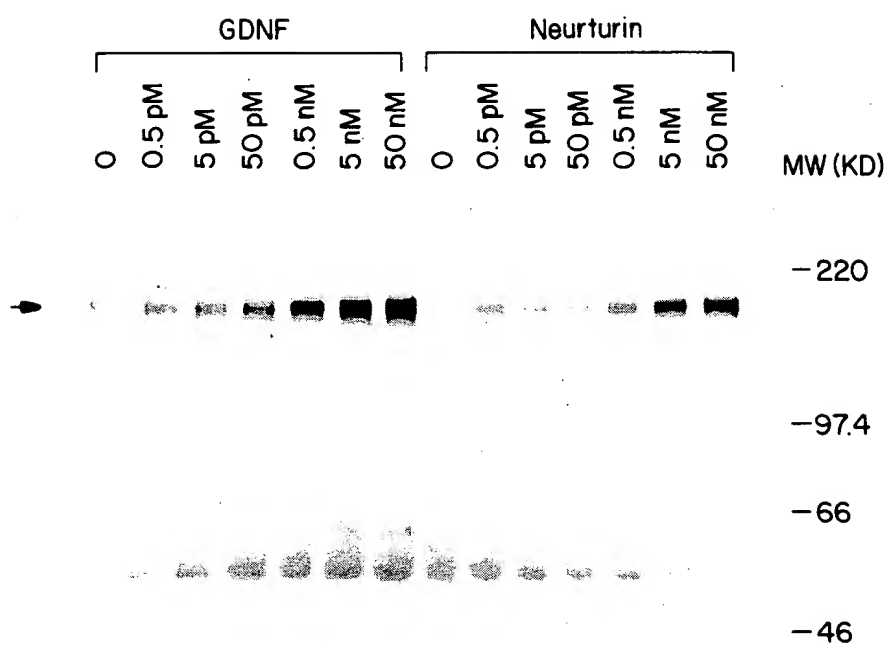


FIG.24

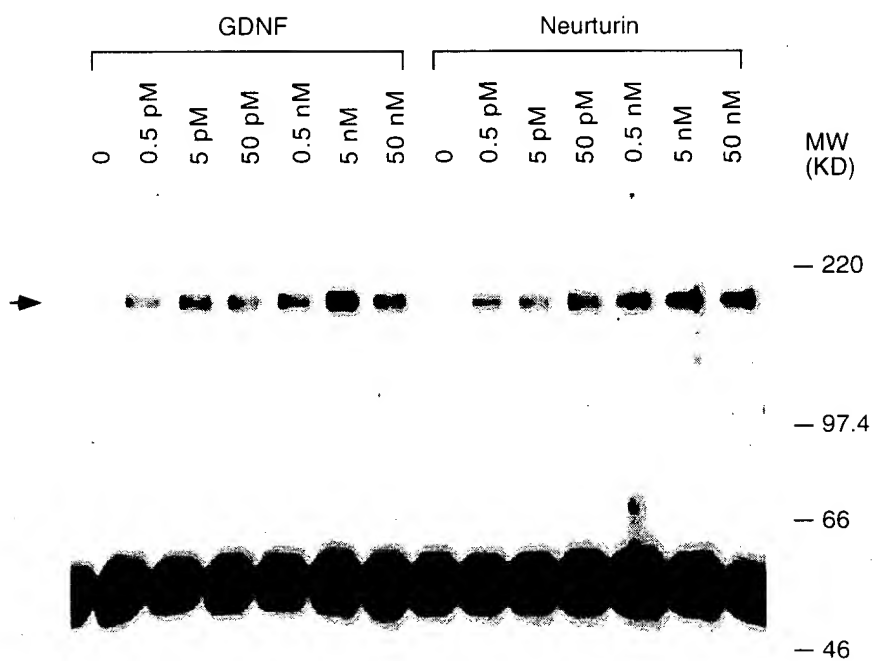
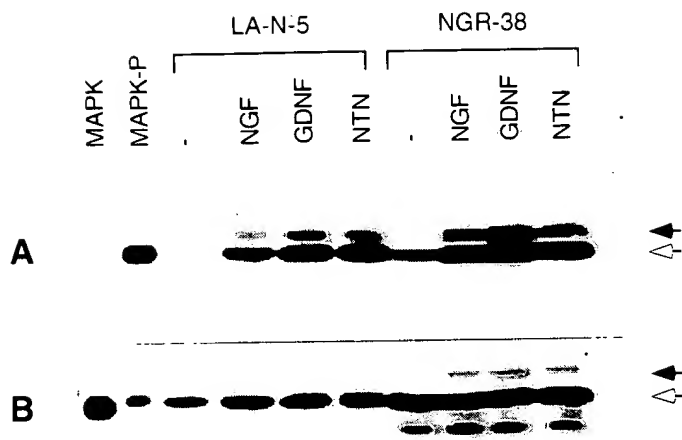


FIG.25





	101		150
CONSENSUS	CKRGMKKE..	CL.IYWS.h. .l..G...le	.SPYE.pvts rlsdier..s
GDNFR	CKRGMKKEKN	CLR.IYWSMYQ	SL.QGNDLLE DSPYE.PVNS RLSDIERAVP
GRR2	CKRGMKKEIQ	CLQ.IYWSIHL	GLTEGEFEFYE ASPYE.PVTS RLSDIERLAS
GRR3	CHRRMKKECAT	QLD.IYWTVHP	VRSLGDYELD VSPYEDTVTS ..K2WKKNLS



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FIG. 20.D

200

CONS	..S....d..	...ksn.	CLd	aKaChLnD.	CkKlRsaYI.	C.....S...e
GDNFR	FISDVFCQVE	HISKGNNCLD	AAKACNLDDT	CKKYSAYIT	PCTTSM	S.NE
GRR2	IFSGTGTDPA	VSTKSNECLD	AAKACNLNDN	CKKLRSSYIS	ICNREIS	PTE
GRR3	KLMLK2D...	....SDLCLK	FAMLCGLNDK	CDRLRKAYGE	AC.....SG.I	

	251					300
CONSENSUS	sve..e.pnc	Ldlrs.Crtcd	.lCRSRLaDF	.tnC.p..r.	t.C.a.ny.	
GDNFR	SYEERERpNC	LSLQDSCKTN	YICRSRLADF	FTNCQPESRS	VSNCLKENYA	
GRR2	SYEDKEKpNC	LDLRSLCRTD	HLCRSRLADF	HANCRASYRT	ITSCPADNYQ	
GRR3	ALPSVA.pNC	LDLRSFCRAD	PLCRSRLMDF	QTHCHPMdIL	GT.C.ATEQS	



## FIG.26C

351	400
CONSENSUS	F..NcCL.nA IqAfng.dv .msq..p... .t.a..... rv...p.l..
GDNR	FKDNTCLKNA IQAFNGGSDV TMWQPAPPVQ TTTTCTTTAF RVKNKP.LGP
GRR2	FTENPCLRNA IQAFNGGTDV NMSPKGPSP ATQAP..... RVEKTPSLPD
GRR3	FSQNPCLMEA IAAKMRFHRO LFSQDWADST FSVMQQQNSS PALRPQ....
401	450
CONSENSUS	..S.....c .v...c...q .q.lk.n.s. ....c.....
GDNR	AGS.ENEIPT HVLPPCANLQ AQKLKSNVSG STELCCLSDSD FGKDGLAGAS
GRR2	DLSDSTSLGT SVITTCSTIQ EQGLKANNNSK ELSMCFTELT TNISPGSKKV
GRR3	.....
451	489
CONSENSUS	.....s..a ..s..l..LP vLmlt.l... 1...l.ets
GDNR	SHITTKSMAA PPSCSLSSLP VLMLTAAL LSVSLAETS
GRR2	IKLNSGSSRA <u>RLSPAALTALP LLMLTLAL</u>
GRR3	..... <u>LRLP VLSPFILTLL LLOTLW</u>